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104204

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Elizabeth (Betsy) Kemmerer
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Searcher: _____
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
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DRLink: _____
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WWW/Internet: _____
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OM protein - protein search, using sw model

Run on: September 23, 2003, 14:58:07 ; Search time 87 Seconds

(without alignments)
259.071 Million cell updates/sec

Title: US-10-004-832-2

Perfect score: 735
Sequence: 1 MDSLIVCEVPELTERLKR.....IRTDLTLTAWLQKLSFPR 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_19Jun03:*

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22: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*
23: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*
24: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	735	100.0	142	AA1981309	Haematopoietic mat
2	735	100.0	142	AA1981309	CBFBOB1 protein s
3	735	100.0	142	AA1981309	Human CBFBOB1 pro
4	735	100.0	142	AA1981309	Human haemopoietic
5	735	100.0	142	AA1981309	Human haemopoietic
6	735	100.0	142	AA1981309	Human haemopoietic
7	699	95.1	147	AA1981309	Lung cancer associ
8	616	83.8	155	AA1981309	Human Gli3 Maturat
9	570	77.6	178	AA1981309	Novel human diagno

10	558	75.9	109	20	AA1981309	Human secreted pro
11	513.5	69.9	126	22	AA1981309	Novel human diagno
12	464.5	63.2	116	21	AA1981309	Human secreted pro
13	376	51.2	141	22	AA1981309	Drosophila melanog
14	247.5	33.7	58	22	AA1981309	Novel human diagno
15	167	22.7	46	22	AA1981309	Novel human diagno
16	154	21.0	113	24	AA1981309	Human DTPP growth
17	148	20.1	27	14	AA1981309	Bovine Gli3 Maturat
18	113	15.4	350	16	AA1981309	Deduced human prot
19	113	15.4	350	23	AA1981309	Human ovarian canc
20	113	15.4	385	21	AA1981309	Human colon cancer
21	113	15.4	385	22	AA1981309	Human colon cancer
22	111.5	15.2	133	21	AA1981309	Arabidopsis thalia
23	111.5	15.2	133	21	AA1981309	Arabidopsis thalia
24	111.5	15.2	133	21	AA1981309	Arabidopsis thalia
25	111.5	15.2	140	21	AA1981309	Arabidopsis thalia
26	111.5	15.2	140	21	AA1981309	Arabidopsis thalia
27	111.5	15.2	170	21	AA1981309	Arabidopsis thalia
28	109.5	14.9	343	22	AA1981309	Drosophila melanog
29	109	14.8	349	22	AA1981309	Human protein SFO
30	109	14.8	349	22	AA1981309	Novel protein kina
31	109	14.8	351	20	AA1981309	MRKAPB control
32	109	14.8	399	22	AA1981309	Human protein SFO
33	108	14.7	132	21	AA1981309	Arabidopsis thalia
34	108	14.7	132	21	AA1981309	Arabidopsis thalia
35	108	14.7	132	21	AA1981309	Arabidopsis thalia
36	108	14.7	139	21	AA1981309	Arabidopsis thalia
37	108	14.7	139	21	AA1981309	Arabidopsis thalia
38	108	14.7	150	21	AA1981309	Arabidopsis thalia
39	108	14.7	348	22	AA1981309	Novel human protei
40	105	14.3	132	21	AA1981309	Arabidopsis thalia
41	105	14.3	132	21	AA1981309	Arabidopsis thalia
42	105	14.3	139	21	AA1981309	Arabidopsis thalia
43	105	14.3	178	21	AA1981309	Arabidopsis thalia
44	104	14.1	132	21	AA1981309	Arabidopsis thalia
45	104	14.1	132	21	AA1981309	Arabidopsis thalia

ALIGNMENTS

RESULT 1	AA1981309	strand: Protein; 142 AA.
ID	AA1981309	
AC	AA1981309	
XX		
DT	22-DEC-1995	(first entry)
XX		
DE	Haematopoietic maturation factor.	
XX		
KW	Haematopoietic maturation factor; cancer; leukemia; hemophilia.	
XX		
OS	Homo sapiens.	
XX		
PN	W09519985-A1.	
XX		
PD	27-JUL-1995.	
XX		
PF	10-MAY-1994;	94WO-US05186.
XX		
PR	25-JAN-1994;	94US-0187186.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Adams MD, Kirkness E, Olsen H, Rosen C;	
XX		
DR	WPI: 1995-269411/35.	
XX		
DR	N-PSDB: AA099843.	
XX		
PT	New DNA encoding human haemopoietic maturation factor - useful in	
XX		
PT	treatment and diagnosis, e.g. of cancer, leukaemia, hemophilia etc.	
XX		

QY 61 LPEROPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMMYAGSKNRLVQTAELTKV 120
 |||||||
 DB 61 LPEROPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMMYAGSKNRLVQTAELTKV 120
 |||||||
 QY 121 FEIRTTDDLTEAMLOEKLSPFR 142
 |||||||
 DB 121 FEIRTTDDLTEAMLOEKLSPFR 142
 |||||||

RESULT 4
 AAY54900
 ID AAY54900 standard; Protein; 142 AA.
 XX
 AC AAY54900;
 XX
 DT 09-FEB-2000 (first entry)
 XX
 DE Human haemopoietic maturation factor protein sequence.
 XX
 KW Haemopoietic maturation factor; HMF; human; HMF; leukaemia; haemolysis;
 KM cell proliferation inhibitor; T-cell proliferation; polycythemia vera;
 KM lymphocyte proliferation; haematopoietic progenitor cell formation;
 KM blood disorder; myelodysplasia; haemophilia; splenomegaly; therapy.
 XX
 OS Homo sapiens.
 XX
 PN US586669-A.
 XX
 PD 16-NOV-1999.
 XX
 PF 16-MAY-1995; 95US-0442497.
 XX
 PR 25-JAN-1994; 94US-0187186.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Olsen HS, Rosen CA, Kirkness EF, Adams MD;
 XX
 DR WPI: 2000-037451/03.
 DR N-PSDB: AAZ37459.
 XX
 PT Haemopoietic maturation factor polypeptide useful for inhibiting
 PT leukaemia cell proliferation, stimulating T-cell proliferation and
 PT differentiation, stimulating thymocyte proliferation and stimulating
 PT haemopoietic progenitor cell formation.
 XX
 PS Claim 1; Fig 1; 27pp; English.
 CC This sequence is the human haemopoietic maturation factor (HMF) of
 CC the invention. The HMF polypeptide is capable of inhibiting leukaemia
 CC cell proliferation, stimulating T-cell proliferation and differentiation,
 CC stimulating thymocyte proliferation and stimulating haematopoietic
 CC progenitor cell formation. HMF is useful for treating leukaemia and other
 CC blood disorders, e.g. haemolysis, polycythemia vera, myelodysplasia,
 CC haemophilia, and splenomegaly, and for inducing differentiation of
 CC immature malignant leukaemia cells. HMF has a narrower range of
 CC activities and greater specificity for functionally differentiated cells
 CC than general growth factors and so can be used to treat diseases specific
 CC for the activities it regulates.
 CC
 XX
 SO Sequence 142 AA;
 Query Match 100.0%; Score 735; DB 21; Length 142;
 Best Local Similarity 100.0%; Pred. No. 6,7e-74;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSDSLVYCEVDPPELTELKRRFRFRKETDAAIIMKVDKRDQMVVLEEFQNIISPEELKME 60
 |||||||
 DB 1 MSDSLVYCEVDPPELTELKRRFRFRKETDAAIIMKVDKRDQMVVLEEFQNIISPEELKME 60
 |||||||
 QY 61 LPEROPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMMYAGSKNRLVQTAELTKV 120
 |||||||

DB 61 LPEROPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMMYAGSKNRLVQTAELTKV 120
 |||||||
 QY 121 FEIRTTDDLTEAMLOEKLSPFR 142
 |||||||
 DB 121 FEIRTTDDLTEAMLOEKLSPFR 142
 |||||||

RESULT 5
 AAE14612
 ID AAE14612 standard; Protein; 142 AA.
 XX
 AC AAE14612;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Human haemopoietic maturation factor.
 XX
 KW Human; haemopoietic maturation factor; HMF; T cell; graft rejection;
 KM autoimmune disease; leukaemia; blood-related disorder; haemolysis;
 KW haemophilia; splenomegaly; malignant.
 XX
 OS Homo sapiens.
 XX
 PN US6346246-B1.
 XX
 PD 12-FEB-2002.
 XX
 PF 15-JUN-1999; 99US-0333033.
 XX
 PR 16-MAY-1995; 95US-0442497.
 XX
 PR 25-JAN-1994; 94US-0187186.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Kirkness EF, Adams MD, Olsen HS, Rosen CA;
 XX
 DR WPI: 2002-224985/28.
 DR N-PSDB: AAD27921.
 XX
 PT New antibody that specifically binds to human haematopoietic maturation
 PT factor polypeptide, useful to prevent T cell expansion for treating
 PT graft rejection and autoimmune diseases.
 XX
 PS Claim 1; Fig 1; 24pp; English.
 CC The invention relates to an antibody that specifically binds to
 CC human haemopoietic maturation factor (HMF). The antibody is useful as an
 CC antagonist of HMF polypeptide, to prevent expansion of T cells which may
 CC be employed for treating conditions related to the presence of T cells
 CC e.g. graft rejection and autoimmune diseases. The antibody
 CC is also useful to isolate HMF polypeptide from tissue expressing the
 CC polypeptide, and in diagnostic assays for detecting altered levels of
 CC the polypeptide in various tissues. The HMF polypeptide and
 CC polynucleotide are utilised for therapeutic purposes, e.g. to treat
 CC leukaemia, blood-related disorders (e.g. haemolysis, haemophilia,
 CC splenomegaly), to stimulate differentiation and proliferation of cells of
 CC haematopoietic or stromal origin, and to remove malignant cells.
 CC The present sequence is human haemopoietic maturation factor.
 CC
 XX
 SO Sequence 142 AA;
 Query Match 100.0%; Score 735; DB 23; Length 142;
 Best Local Similarity 100.0%; Pred. No. 6,7e-74;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSDSLVYCEVDPPELTELKRRFRFRKETDAAIIMKVDKRDQMVVLEEFQNIISPEELKME 60
 |||||||
 DB 1 MSDSLVYCEVDPPELTELKRRFRFRKETDAAIIMKVDKRDQMVVLEEFQNIISPEELKME 60
 |||||||
 QY 61 LPEROPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMMYAGSKNRLVQTAELTKV 120
 |||||||
 DB 61 LPEROPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMMYAGSKNRLVQTAELTKV 120
 |||||||

QY 121 FEIRTTDDLTEAWLQEKLSFFR 142
 DB 121 FEIRTTDDLTEAWLQEKLSFFR 142

RESULT 6
 ABG74162
 ID ABG74162 standard; Protein: 142 AA.

XX ABG74162;

XX 06-MAY-2003 (first entry)

XX Human haemopoietic maturation factor.

XX Human; haemopoietic maturation factor; HMF; haemopoiesis; bone marrow;
 KW stromal cell differentiation; mature blood cell differentiation; HIV;
 KW T cell proliferation; T cell differentiation; gene therapy; leukaemia;
 KW anaemia; thrombocytopenia; granulocytopenia; blood-related disorder;
 KW haemolysis; polycythemia vera; haemophilia; T cell deficiency disease;
 KW immature malignant leukaemia cell differentiation; graft rejection;
 KW haematopoietic cell precursor replacement; bone marrow transplant;
 KW autoimmune disease.

XX Homo sapiens.

XX US2002146408-A1.

XX 10-OCT-2002.

XX 07-DEC-2001; 2001US-0004832.

XX 16-MAY-1995; 95US-0442497.

XX 15-JUN-1999; 99US-0333033.

XX 25-JAN-1994; 94US-0187186.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Kirtness EF, Adams MD, Olsen HS, Rosen CA;

XX WPI; 2003-228012/22.

XX N-PSDB; ABX16160.

XX New isolated hemopoietic maturation factor polypeptide useful for

XX stimulating hemopoiesis, for treating leukemia, anemia,

XX thrombocytopenia, and granulocytopenia.

XX Claim 16; Fig 1; 27pp; English.

XX The invention relates to an isolated haemopoietic maturation factor (HMF)
 CC polypeptide encoded by DNA of American Type Culture Collection (ATCC)
 CC Deposit No. 75514, and their fragments, analogues or derivatives. The
 CC polypeptide is useful for treating a patient having a need of HMF. The
 CC polypeptide and a host cell genetically engineered with the polypeptide
 CC are useful for identifying compounds active as agonists or antagonists to
 CC HMF. The nucleic acid encoding the polypeptide is useful for diagnosing a
 CC disease or susceptibility to a disease related to the underexpression of
 CC HMF. A host cell genetically engineered with the nucleic acid is useful
 CC for treating a patient having the need to inhibit HMF. The polypeptide is
 CC used in a diagnostic process by analysing for the presence of the
 CC polypeptide in a sample from a host. The polypeptide is useful for
 CC treating leukaemia, anaemia, thrombocytopenia and granulocytopenia, other
 CC blood-related disorders e.g. haemolysis, polycythemia vera, haemophilia
 CC and diseases caused by T cell deficiencies e.g. leukaemia and human
 CC immunodeficiency virus (HIV) infection. The polypeptide stimulates
 CC differentiation of immature malignant leukaemia cells. The polypeptide
 CC can be used to offset the destruction of haematopoietic cell precursors
 CC which occurs during radiation or chemotherapy by expanding the stromal
 CC cell population and the subsequent expansion of haematopoietic cells and
 CC stimulates the differentiation of mature blood cells in situations where
 CC a patient has undergone a bone marrow transplant. The polypeptide is also
 CC useful for stimulating bone marrow/haematopoietic cells in vitro for gene
 CC therapy purposes, for stimulation of bone marrow recovery due to

CC chemotherapy, for stimulating proliferation and differentiation of
 CC certain human T cell populations. The nucleic acid is useful as a probe
 CC for a cDNA library to isolate other genes which have high sequence
 CC similarity to the HMF gene or other similar biological activity and for
 CC chromosomal identification. A compound which inhibits the polypeptide is
 CC useful for preventing expansion of T cell populations, for treating
 CC conditions such as graft rejection and autoimmune diseases. The present
 CC sequence represents the amino acid sequence of human haemopoietic
 CC maturation factor.

XX Sequence 142 AA;

XX Query Match 100.0%; Score 735; DB 24; Length 142;

XX Best Local Similarity 100.0%; Pred. No. 6,7e-74;

XX Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSDSLVYCEVDEPTELTKRFRKEFDNAIIMKVKDKRMVYLEEFONISPEELKME 60

DB 1 MSDSLVYCEVDEPTELTKRFRKEFDNAIIMKVKDKRMVYLEEFONISPEELKME 60

QY 61 LPERQPRFVYVSYKYVHDDGRVSPICFIFSSPVGCKPEQOMYVAGSKNRLVOTAEPLTKV 120

DB 61 LPERQPRFVYVSYKYVHDDGRVSPICFIFSSPVGCKPEQOMYVAGSKNRLVOTAEPLTKV 120

QY 121 FEIRTTDDLTEAWLQEKLSFFR 142

DB 121 FEIRTTDDLTEAWLQEKLSFFR 142

RESULT 7
 AAB58304
 ID AAB58304 standard; Protein: 147 AA.

XX AAB58304;

XX 14-MAR-2001 (first entry)

XX Lung cancer associated polypeptide sequence SEQ ID 642.

XX Human; lung cancer associated protein; neuroprotective; cytostatic;
 KW cardiocactive; immunomodulatory; muscular active; vunerary;
 KW gastrointestinal; nephrotoxic; antiinfective; gynecological;
 KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
 KW proliferative disorder; wound healing; infectious disease.

XX Homo sapiens.

XX WO200055180-A2.

XX 21-SEP-2000.

XX 08-MAR-2000; 2000WO-US05918.

XX 12-MAR-1999; 99US-0124270.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (ROSE/) ROSEN C A.

XX Ruden SM;

XX WPI; 2000-587514/55.

XX N-PSDB; AAF18180.

XX Lung cancer associated gene sequences, referred to as lung cancer

XX antigens, useful for treatment, prevention, and diagnosis of disorders

XX such as lung cancer -

XX Claim 11; Page 1140-1141; 1425pp; English.

XX polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer

XX associated proteins represented in AAB58106 - AAB58548. Lung cancer

XX associated proteins and polynucleotide sequences, their agonists, and

XX antagonists may have neuroprotective; cytostatic; cardioactive;

DR N-PSDB; AAQ53862

PT responsible for genetic disorders or other traits and to assess biodiversity -

xx		Claim 20; SEQ ID NO 50286; 103pp; English.
-ps		
cc	The invention relates to isolated polynucleotide (I) and	
cc	polypeptide (II) sequences. (I) is useful as hybridisation probes,	
cc	polymerase chain reaction (PCR) primers, oligomers, and for chromosome	
cc	and genome mapping, and in recombinant production of (II). The	
cc	polynucleotides are also used in diagnostics as expressed sequence tags	
cc	for identifying expressed genes. (I) is useful in gene therapy techniques	
cc	to restore normal activity of (II) or to treat disease states involving	
cc	(II). (II) is useful for generating antibodies against it, detecting or	
cc	quantitating a polypeptide in tissue, as molecular weight markers and as	
cc	a food supplement. (II) and its binding partners are useful in medical	
cc	imaging of sites expressing (II). (I) and (II) are useful for treating	
cc	disorders involving aberrant protein expression or biological activity.	
cc	The polypeptide and polynucleotide sequences have applications in	
cc	diagnostics, forensics, gene mapping, identification of mutations	
cc	responsible for genetic disorders or other traits to assess biodiversity	
cc	and to produce other types of data and products dependent on DNA and	
cc	amino acid sequences. ABG00010-ABG30377 represent novel human	
cc	diagnostic amino acid sequences of the invention.	
cc	Note: The sequence data for this patent did not appear in the printed	
cc	specification, but was obtained in electronic format directly from WIPO	
cc	at ftp.wipo.int/pub/published_pcl_sequences.	
xx		
sq	Sequence 178 AA;	
OY	Query Match 77.6%; Score 570; DB 22; Length 178;	
Dd	Best Local Similarity 84.1%; Pred. No. 2,3e-55;	
OY	Matches 122; Conservative 2; Mismatches 15; Indels 6; Gaps 5	
Dd	2 SDSLVCCVDPELLEKLRFRFKETDNAAILMKVKDR-QMVLLEEFQNISPE-ELKM 59 25 SDSLAVCCVDDELTEKLKRFRFKETDNAAILMKDKRGQMVLVEEFOINSPORELKM 84 	
OY	60 ELPER-OEPFVYSKYKVHDDGRVSYPLCFIF-SSPVCCKPQQOMVVGSKNRILVOTAEI 117 - - : 85 GFPRDRAKRFVYSKYKVHDDGRVSYPLCFIFPPRPVCGKPEQQMMYIGSKNRLVOTAEI 144 	
OY	118 TKVFIEIRTYDDL-T-EANVLOEKLSF 140 	
Dd	145 TKGVPKSRTYXLTSLRPMWJQEKLSF 169 	
RESULT 10		
AAAY36208		
ID	AAAY36208 standard; protein; 109 AA.	
XX	AAAY36208;	
XX		
DT	23-SEP-1999 (first entry)	
XX		
DE	Human secreted protein #80.	
XX		
KW	Secreted protein; human; cytosolic; thrombotic; osteopathic; forensic;	
XV	diagnostic; gene therapy; chromosome mapping; secretion vector.	
XX		
OS	Homo sapiens.	
XX		
PN	WO925825-A2.	
XX		
PD	27-MAY-1999.	
XX		
PF	13-NOV-1998; 98WO-IBO1862.	
XX		
PR	04-SEP-1998; 98US-0099273.	
PR	13-NOV-1997; 97US-006677.	
PR	17-DEC-1997; 97US-0069957.	
PR	09-FEB-1998; 98US-0074121.	
PR	13-APR-1998; 98US-0081563.	
PR	10-AUG-1998; 98US-0096116.	
PA	(GEST) GENSET.	

XX	Bougueleret L, Duclert A, Dumas Milne Edwards J;
PI	
XX	WPI: 1999-347472/29.
DR	N-PSDB: AAX97892.
XX	
PT	Extended cDNAs encoding secreted proteins
XX	
PS	Claim 7, Page 302, 307pp; English.
XX	
CC	AAY36129-Y36222 represent novel human secreted proteins encoded by the
CC	extended cDNA sequences represented in AAX97813-X97906. The proteins
CC	of the invention have cytosolic, thrombotic and osteopathic activity.
CC	The extended cDNAs can be used to express secreted proteins or parts of
CC	them or to obtain antibodies capable of binding to the secreted
CC	proteins. They may also be used in diagnostic, forensic, gene therapy
CC	and chromosome mapping procedures. Uses also include design of
CC	expression vectors and secretion vectors.
XX	
SQ	Sequence 109 AA;
	Query Match 75.9%; Score 558; DB 20; Length 109;
	Best Local Similarity 98.2%; Pred. No.2.6e-54;
	Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY	34 MKVKDKRQMVVLEEFQNIISPEELKMLPERQPRFVVSXYKVHDDGRVSYPLCFIFSSP 93
Db	1 MKVKDKRQMVVLEEFQNIISPEELKMLPERQPRFVVSXYKVHDDGRVSYPLCFIFSSP 60
QY	94 VGCPPEQDMYAGSKNRLVQTAELTKVEIRTTDDLTFAMLOEKISFFR 142
Db	61 VGCPPEQDMYAGSKNRLVQTAELTKVEIRTTDDLTFAMLOEKISFFR 109
RESULT 11	
ABG19926	
ID	ABG19926 standard; Protein; 126 AA.
XX	
AC	ABG19926;
XX	
DT	18-FEB-2002 (first entry)
XX	
DE	Novel human diagnostic protein #19917.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW	food supplement; medical imaging; diagnostic; genetic disorder.
XX	
OS	Homo sapiens.
XX	
PN	WO200175067-A2.
XX	
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001WO-US08631.
XX	
PR	31-MAR-2000; 2000US-0540217.
PR	23-AUG-2000; 2000US-0649167.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Drimnac RT, Liu C, Tang YT;
XX	
DR	WPI: 2001-639362/73.
DR	N-PSDB: AAS84113.
XX	
PT	New isolated polynucleotide and encoded polypeptides, useful in
PT	diagnostics, forensics, gene mapping, identification of mutations
PT	responsible for genetic disorders or other traits and to assess
PT	biodiversity -
XX	
PS	Claim 20; SEQ ID No 50285; 103pp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and

polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention. CC Note: The sequence data for this patent did not appear in the printed CC specification, but was obtained in electronic format directly from WIPO CC at [ftp.wipo.int/pub/published_pct_sequences](http://wipo.int/pub/published_pct_sequences). CC

Query Match	69.9%	Score 513.5;	DB 22;	Length 126;
Best Local Similarity	78.5%	Pred. No. 2.9e+49;		
Matches 106; Conservative	0;	Mismatches 4;	Indels 25;	Gaps 2;

```

QY 1 MSLSLVCCVDEDELTEKLRKFRKRETDNAIIMKVDKROMVYLLEEFQIISPEELKME 60
Db 6 MSSSLVCCVDEDELTEKLRKFRKRETDNAIIMKVDKROMVYLLEEFQ----- 55
QY 61 LPBQRPVYVSKYVHDDGRVSYPLCFIFSSPYGCKPEQOMYAGSKNRLVOTAEITKY 120
Db 56 -----FVYVSIKTVHDDGRVSYPLCFIFSSPYGCKPEQOMYAGSKTRLVOTAEITKY 108
QY 121 FEIRTTDDLTEAMLQ 135
Db 109 -----QTGMMLQ 115

```

PT	New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PI	obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX	diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX	
DR	N-PSDB; AAC03959.
DR	
XX	
XX	
PA	(G E S T) G E N S E T .
XX	
PI	Dumas Milne Edwards J, Duclert A, Giordano J;
XX	
XX	WPI; 2000-500381/45.
XX	
XX	
PR	26-FEB-1999; 99US-0122487.
XX	
XX	
PD	06-SEP-2000.
PN	
PN	EP1033401-A2.
XX	
OS	Homo sapiens.
XX	
KM	Human; 5' EST; expressed sequence tag; secreted protein; CDNA isolation,
KW	gene therapy; chromosome mapping.
XX	
DE	
XX	
XX	Human secreted protein, SEQ ID NO: 8034.
DT	
DT	06-OCT-2000 (first entry)
XX	
AC	AAG03953;
XX	
ID	AAG03953 standard; Protein; 116 AA.
RESULT 12	
AAG03953	

XX	
PS	Claim 13; SEQ ID 8034; 71pp + CD-ROM; English.

CC The present sequence is a polypeptide encoded by one of a large number
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC were prepared from total human RNAs or polyA+ RNAs derived from 30
CC different tissues. EST sequences usually correspond mainly to the 3'
CC untranslated region (UTR) of the mRNA because they are often obtained
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC those cases where longer cDNA sequences have been obtained, the full 5'
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC ends and can therefore be used to obtain full length cDNAs and genomic
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC chromosome mapping procedures. They are used to obtain upstream
CC regulatory sequences and to design expression and secretion vectors.

Sequence	116 AA;
Query Match	63.2%;
Best Local Similarity	79.3%;
Matches	88; Conservative
	13; Mismatches
	9; Indels
	1; Gaps
	1.

```

Oy  M S D S L V C E P D P E T L K R F R F R K E D N A I I M K D X R O M V L E E E P O N S I P E L K A E 60
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db  1 M S S L X A C D V A E D I V E L K R F R F R K E T N N A I I M K I D X R L V D D E L E G I S P D L K A E 60

Oy
Db
Oy  61 L P E K O P R - F V Y I S K Y I V H D D G R V S Y P L C T F F S S P V C K E D Q O M M T A G S K N R 110
    1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db  61 L P E K O P T F F V I S K Y O H D D G R V S Y P L C T F F S S P V C K E E D Q O M M A T A G S K N R 111

```

RESULT 13	
ABB61879	
ID	ABB61879 standard; Protein; 141 AA.
XX	
XX	
AC	ABB61879;
XX	
DT	26-MAR-2002 (first entry)
XX	
DE	Drosophila melanogaster polypeptide SEQ ID NO 12429.
XX	
KW	Drosophila; developmental biology; cell signalling; insecticide;
KW	pharmaceutical.
XX	
OS	Drosophila melanogaster.
XX	
PN	WO200171042-A2.
XX	
PD	27-SEP-2001.
XX	
PF	23-MAR-2001; 2001MO-US09231.
XX	
PR	23-MAR-2000; 2000US-191657P.
XX	
PR	11-JUL-2000; 2000US-0614150.
XX	
PA	(PEKE) PE CORP NY.
XX	
PI	Venter JC, Adams M, Li PWD, Myers EW;
XX	
DR	WPI; 2001-656860/75.
DR	N-PSDB; ABL05982.
PT	New isolated nucleic acid detection reagent for detecting 1000 or more
PT	genes from Drosophila and for elucidating cell signalling and cell-cell
PT	interactions -
PS	
PS	Disclosure; SEQ ID NO 12429; 21pp + Sequence Listing; English.
XX	
CC	
CC	The invention relates to an isolated nucleic acid detection reagent
CC	capable of detecting 1000 or more genes from Drosophila. The invention
CC	is
CC	useful in developmental biology and in elucidating cell signalling and
CC	cell-cell interactions in higher eukaryotes for the development of

CC	quantitating a polypeptide in tissue, as molecular weight markers and as
CC	a food supplement. (II) and its binding partners are useful in medical
CC	imaging of sites expressing (II). (I) and (II) are useful for treating
CC	disorders involving aberrant protein expression or biological activity.
CC	The polypeptide and polynucleotide sequences have applications in
CC	diagnostics, forensics, gene mapping, identification of mutations
CC	responsible for genetic disorders or other traits to assess biodiversity
CC	and to produce other types of data and products dependent on DNA and
CC	amino acid sequences. ABG00010-ABG30377 represent novel human
CC	diagnostic amino acid sequences of the invention.
CC	Note: The sequence data for this patent did not appear in the printed
CC	specification, but was obtained in electronic format directly from WIPO
CC	at ftp.wipo.int/pub/published_pct_sequences.
CC	
XX	Sequence 58 AA:
XX	
XX	Query Match 33.7%; Score 247.5; DB 22; Length 58;
XX	Best Local Similarity 45.7%; Pred. No. 4.8e-20;
XX	Matches 58; Conservative 0; Mismatches 0; Indels 69; Gaps 1;
XX	
QY	16 EKLRRFRKRTDAAITIMKYDKRQNVLEEFQNSPEELKMLPERQPRFVVSYYK 75
DB	1 EKLRRFRKRTDAAITIMKYDKRQNVLEEFQNSPEELKMLPERQPRFVVSYYK 35
QY	76 VHDGRVSYPLCLFIFSSVGCPRQQAIVAGSKRLVQTALTYVFIRITDDLTFAWLQ 135
DB	36 -----VFIRITDDLTFAWLQ 51
QY	136 EKLSFPR 142
DB	52 EKLSFPR 58
XX	
XX	RESULT 15
XX	ABG19925
XX	ID ABG19925 standard; Protein: 46 AA.
XX	ABG19925;
XX	18-FEB-2002 (first entry)
XX	Novel human diagnostic protein #19916.
XX	Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX	food supplement; medical imaging; diagnostic; genetic disorder.
XX	Homo sapiens.
XX	WO200175067-A2.
XX	11-OCT-2001.
XX	30-MAR-2001; 2001WO-US08631.
XX	31-MAR-2000; 2000US-0540217.
XX	23-AUG-2000; 2000US-0649167.
XX	(HYSE-) HXSEQ INC.
XX	Drmanac RT, Liu C, Tang YT;
XX	WPI; 2001-639362/73.
XX	N-PSDB; AAS84112.
XX	New isolated polynucleotide and encoded polypeptides, useful in
XX	diagnostics, forensics, gene mapping, identification of mutations
XX	responsible for genetic disorders or other traits and to assess
XX	biodiversity
XX	Claim 20; SEQ ID No 50284; 103pp; English.
XX	The invention relates to isolated polynucleotide (I) and
XX	polypeptide (II) sequences. (I) is useful as hybridisation probes,

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG03377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 46 AA;

Query Match 22.7%; Score 167; DB 22; Length 46;
 Best Local Similarity 97.1%; Pred. No. 3.3e-11;
 Matches 33; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 34 MKVVDKROMVLEEFONISPEELKMLPERQPR 67
 ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1 MKVVDKROMVLEEFONISPEELKMLPERQPR 34

Search completed: September 23, 2003, 15:08:48
 Job time : 89 secs

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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:06:08 ; Search time 41 Seconds
(without alignments)
335.072 Million cell updates/sec

Title: US-10-004-832-2

Perfect score: 735

Sequence: 1 MSDSLVCEVPELLEKLRK.....IRTTDDLTEAMLOEKLSFPR 142

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	686	93.3	142	2 JC7218	gila maturation fa
2	622	84.6	142	1 PT0410	gila maturation fa
3	617	83.9	141	1 JDBOB	gila maturation fa
4	611	83.1	141	1 S22149	gila maturation fa
5	349	47.5	138	2 JC6308	gila maturation fa
6	175	23.8	141	2 T37877	cofilin/tropomyosi
7	123.5	16.8	328	2 T40910	probable tyrosine
8	116.5	15.9	149	2 S54047	hypothetical prote
9	113	15.4	350	2 A55922	tyrosine kinase A6
10	111.5	15.2	140	2 T01232	actin-depolymerizi
11	111.5	15.2	140	2 A86149	actin-depolymerizi
12	109	14.8	139	2 S30935	actin-depolymerizi
13	109	14.8	349	2 T46362	probable tyrosine
14	106.5	14.5	357	2 T30015	probable tyrosine
15	103.5	14.1	133	2 T47539	actin depolymerizi
16	100.5	13.7	130	2 T05788	actin-depolymerizi
17	97.5	13.3	142	2 S71361	actin-binding prot
18	95.5	13.0	130	2 T05675	actin-depolymerizi
19	95	12.9	130	2 T47540	actin-depolymerizi
20	93	12.7	132	2 G64717	actin depolymerizi
21	92.5	12.6	137	2 T43245	actin depolymerizi
22	91	12.4	126	2 S30934	probable actin-dep
23	91	12.4	1289	2 F72308	actin-depolymerizi
24	90.5	12.3	332	2 S64375	hypothetical prote
25	85.5	11.6	139	2 T02914	probable tyrosine
26	84	11.4	132	2 B45543	actin-depolymerizi
27	82.5	11.2	166	1 S12632	actin depolymerizi
28	82.5	11.2	166	1 S12584	cofilin - human
29	82.5	11.2	166	2 S49101	cofilin - rat

30	80.5	11.0	166	1 A29240	cofilin - pig
31	80.5	11.0	427	2 B71466	hypothetical prote
32	80.5	11.0	520	2 F70350	recombination prot
33	79	10.7	165	1 A35702	desitin - chicken
34	78.5	10.7	166	1 A35812	cofilin - chicken
35	77.5	10.5	139	2 T02883	actin-depolymerizi
36	77.5	10.5	379	2 T34100	hypothetical prote
37	77	10.5	771	2 H69305	signal-transducing
38	76.5	10.4	609	2 S57378	hypothetical prote
39	76	10.3	139	2 T02882	actin-depolymerizi
40	76	10.3	875	2 JC5186	DNA-directed DNA p
41	75.5	10.3	165	1 A54184	desitin [validated
42	75.5	10.3	165	1 A55179	desitin - pig
43	75.5	10.3	166	1 B35703	cofilin - chicken
44	75.5	10.3	349	2 B83973	hypothetical prote
45	75.5	10.3	510	2 T20276	hypothetical prote

ALIGNMENTS

```

RESULT 1
JC7218
gila maturation factor-gamma - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 02-Nov-2001
C:Accession: JC7218
R:Tsukikl, H.; Asai, K.; Yamamoto, M.; Fujita, K.; Inoue, Y.; Kawai, Y.; Tada, T.; Mor
J. Biochem. 127, 517-523, 2000
A:Title: Cloning of a rat gila maturation factor-gamma(RGMEG) cDNA and expression of
A:Reference number: JC7218; MUID:20198266; PMID:10731725
A:Accession: JC7218
A:Molecule type: mRNA
A:Residues: 1-142 <TSU>
C:Comment: This factor is a regulator of signal transduction with many phosphorylatio
C:Superfamily: gila maturation factor beta
C:Keywords: differentiation

Query Match          93.3%; Score 686; DB 2; Length 142;
Best Local Similarity 91.5%; Pred. No. 1.6e-56;
Matches 130; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY      1 MSDSLVCEVPELLEKLRKFRPREPDNNAITKKVDROMVYLEEFQNSPELKE 60
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 MSDSLVCDVPELKEITLKRFRKRNNAITKKVDROMVYLEEFQNSPELKE 60
QY      61 LPERQPREVVSYKXVHDDGRVSYPLCFIFSSPYGCKPEQDMYAGSKNRLVQTAELTKV 120
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      61 LPERQPREVVSYKXVHDDGRVSYPLCFIFSSPYGCKPEQDMYAGSKNRLVQIAELTKV 120
QY      121 FEIRTTDDLTEAMLOEKLSFPR 142
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB      121 FEIRTTDDLTEAMLOEKLSFPR 142

RESULT 2
PT0410
gila maturation factor beta - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999
C:Accession: PT0410
R:Kaplan, R.; Zahoor, A.; Jaye, M.; Lim, R.
J. Neurochem. 57, 483-490, 1991
A:Title: Molecular cloning and expression of biologically active human gila maturation
A:Reference number: PT0410; MUID:91303115; PMID:1712830
A:Accession: PT0410
A:Molecule type: mRNA
A:Residues: 1-142 <KAP>
A:Cross-references: GB:M66492; GB:M31742; NID:q183369; PIDN:AAA5614.1; PID:q183370
C:Comment: This protein promotes the differentiation of normal neurons and glial cell
C:Genetics:
A:Gene: GDB:GMFB
A:Cross-references: GDB:134671

```


Db 1 MSESEAMFTISDPTMKMEIDFRRLRLKKSVMYAFILKVKATKATEIYVDSGIMDLQSTEEVA 60
 QY 59 MELPEROPRFVYVSYKYVHDDGRVSYPLCFIFSSPYGCKPEQOMMYAGSKNRLVOTAEYL 118
 61 DELSEFNPRFLIVSYPTKTGTGRLSTPLFMIVWRPSATFNDLSMTIYASAKVMFQDVQVH 120
 QY 119 KYFEIRTTDDLTETAMLOEKL 138
 121 KYFEARSDSDITSEAVDEFL 140

RESULT 7

T40910
 Probable tyrosine kinase - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Dec-2002
 C:Accession: T40910
 R:Murphy, L.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
 submitted to the EMBL Data Library, December 1998
 A:Reference number: Z21956
 A:Accession: T40910
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-328 <MUR>
 A:Cross-references: EMBL:AL034490; PIDN:CAA22475.1; GSPDB:GN00068; SPDB:SPCC126.06
 C:Experimental source: strain 97zh-; cosmid c126
 C:Genetics:
 A:Gene: SPDB:SPCC126.06
 A:Map position: 3
 A:introns: 9/1; 35/1; 157/3; 200/3; 246/1; 285/3
 C:Superfamily: probable tyrosine kinase

Query Match 16.8%; Score 123.5; DB 2; Length 328;
 Best Local Similarity 29.5%; Pred. No. 0.00059;
 Matches 39; Conservative 28; Mismatches 50; Indels 15; Gaps 7;

QY 6 VVCEVDPELTETKLRFRFRKEDNNAIMKVKDKQMVLEEFQONISPEELKMLPERQ 65
 174 VAMSTDDKALKALSD--LKSTENMLVILSIDK--EVLISQEKQNIIPSDVKSFFSSSTE 229
 QY 66 PRFVYVSYKYVHDDGRVSYPLCFIFSSPYGCKPEQOMMYAGSKNRLVOT--AELTKVEE- 122
 230 PWFARVYS--LPKDG--SSKILFIYICPMQATVKRMVSSSKLGLDSIKRELGLIVDG 284
 QY 123 -IRITD--DLTE 131
 285 KIESNDADITE 296

RESULT 8

S54047
 Hypothetical protein YDR063w - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein D4245; hypothetical protein D4249; hypothetical
 C:Species: Saccharomyces cerevisiae
 C:Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 19-Apr-2002
 C:Accession: S54047; S58843; S61752; S67879
 R:Hunt, S.; Bowman, S.; Harris, D.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S54031
 A:Accession: S54047
 A:Molecule type: DNA
 A:Residues: 1-149 <HUN>
 A:Cross-references: EMBL:Z49209; NID:g798897; PIDN:CAA89092.1; PID:g798914
 R:Brandt, P.; Otto, B.; Ramlow, S.; Blocker, H.
 submitted to the EMBL Data Library, January 1995
 A:Reference number: S58832
 A:Accession: S58843
 A:Molecule type: DNA
 A:Residues: 1-149 <BRA>
 A:Cross-references: EMBL:X84162; NID:g706817; PIDN:CAA58979.1; PID:g706829
 R:Brandt, P.; Ramlow, S.; Otto, B.; Blocker, H.
 yeast 12, 85-90, 1996

A:Title: Nucleotide sequence analysis of a 32,500 bp region of the right arm of Sacch
 A:Reference number: S61741; MUID:96581250; PMID:8789263
 A:Accession: S61752
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-149 <BRN>
 A:Cross-references: EMBL:X84162; NID:g706817; PIDN:CAA58979.1; PID:g706829
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
 R:Blocker, H.; Brandt, P.
 submitted to the Protein Sequence Database, July 1996
 A:Reference number: S67587
 A:Accession: S67879
 A:Molecule type: DNA
 A:Residues: 1-149 <BLD>
 A:Cross-references: EMBL:Z74359; NID:g1431514; PIDN:CAA98881.1; PID:g1431515; MIPS:YD
 A:Experimental source: strain S288C
 C:Genetics:
 A:Cross-references: SGD:S0002470
 A:Map position: 4R
 C:Superfamily: g1a maturation factor beta

Query Match 15.9%; Score 116.5; DB 2; Length 149;
 Best Local Similarity 27.7%; Pred. No. 0.001;
 Matches 39; Conservative 30; Mismatches 61; Indels 11; Gaps 6;

QY 9 EVDPELTETKLRFR-FKRETDN-AALIMKVD-KDKQMVLEEFQONISPE-----ELKME 60
 6 KIGTETRNKKIKKIFRTSTRTDSTIKALSIKIEKPSYEIVDEDEEDELDELSELAEI 65
 QY 61 IPEROPRFVYVSYKYVHDDGRVSYPLCFIFSSPYGCKPEQOMMYAGSKNRLVOTAEYLTK 119
 66 LPDNPFRVLRVLRPTTADGKQTPVLVYKPMVVSQEKMLYAGALEMIRECGTFK 125
 QY 120 VFEIRT--TDDLTETAMLOEKL 138
 126 LIEVSSGLEDDSDVEELREQL 146

RESULT 9

A55922
 Tyrosine kinase A6 - human
 C:Species: Homo sapiens (man)
 C:Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 09-Dec-2002
 C:Accession: A55922
 R:Beeler, J.F.; Larochele, W.J.; Chedid, M.; Tronick, S.R.; Aaronson, S.A.
 Mol. Cell. Biol. 14, 982-988, 1994
 A:Title: Prokaryotic expression cloning of a novel human tyrosine kinase.
 A:Reference number: A55922; MUID:94119116; PMID:7507208
 A:Accession: A55922
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-350 <BEE>
 A:Cross-references: GB:U02680; NID:g451481; PIDN:MAC50062.1; PID:g451482
 C:Superfamily: probable tyrosine kinase

Query Match 15.4%; Score 113; DB 2; Length 350;
 Best Local Similarity 26.4%; Pred. No. 0.006;
 Matches 38; Conservative 33; Mismatches 53; Indels 20; Gaps 7;

QY 6 VVCEVDPELTETKLRFRFRKEDNNAIMKVKDKQMVLEEFQONISPEELKMLPERQ 65
 178 VAFPSRKAFOALELNNKQLN---YVLEIDIKNEIIL-----ANTNTTELK-DLPKRI 229
 QY 66 P---RFVYVSYKYVHDDGRVSYPLCFIFSSP-VGCKPEQOMMYAGSKNRLVOTAE--- 116
 230 PKDSARVHGFLLYKSH-EGDYLESIVFIYSMPGYCISIREMLVSSCKSLLEIVERQLQ 288
 QY 117 --LTKVEIRTTDDLTETAMLOEKL 138
 289 MDVIRKIEIDNGDELTADFLYEYV 312

RESULT 10

Db 293 KKEIGDGAELTAFLYDEV 312

RESULT 14

T30015

probable tyrosine kinase F38E9.5 [similarity] - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Dec-2002

C:Accession: T30015

R:Wu, X.; Gattung, S.

submitted to the EMBL Data Library, January 1996

A:Description: The sequence of C. elegans cosmid F38E9.

A:Reference number: 220722

A:Accession: T30015

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-357 <WUX>

A:Cross-references: EMBL:U46668; PIDN:AAA93345.1; CESP:F38E9.5

C:Genetics:

A:Gene: CESP:F38E9.5

A:Introns: 9/1; 83/2; 123/3; 169/3; 197/3; 248/1; 288/3; 312/3

C:Superfamily: probable tyrosine kinase

Query Match

Best Local Similarity 14.5%; Score 106.5; DB 2; Length 357;

Best Local Similarity 22.8%; Pred. No. 0.025;

Matches 37; Conservative 30; Mismatches 60; Indels 35; Gaps 5;

QY 6 VVCEVDPELTERKFRFRKFTDAAIIMKYDKDRQVYLEEFQNIISPEELKMELEPERQ 65

Db 171 VAFPVDRNAEALROLASQ--LSFVQLSVDTLNEAIKLEGTLSLEPSQLASKVPRDK 227

QY 66 PREVVYSKYVHDDGRVSPPLCFIFSSP-VGCKPEQOMYAGSKNRLVQTAE----- 116

Db 228 PRITYNEDHW-EGVPOOCTLFIVSLPSSGSSIKERMLYSSCKGPFLSAONQYGVIT 286

QY 117 -----LTKVFEIR-----TTDDLTEAMLOE 136

Db 287 NKFLGRSKMKFKIREKIFLRLKNDMEVDARDLSKALLE 328

RESULT 15

T47539

actin depolymerizing like protein - Arabidopsis thaliana

N:Alternate names: protein F16L2.200

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000

C:Accession: T47539

R:Jordan, N.; Bangert, S.; Wiedemann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.;

submitted to the Protein Sequence Database, March 2000

A:Reference number: 224468

A:Accession: T47539

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-133 <JOR>

A:Cross-references: EMBL:AL162459

A:Experimental source: cultivar Columbia; BAC clone F16L2

C:Genetics:

A:Map position: 3

A:Introns: 43/1; 84/2

A:Note: F16L2.200

C:Superfamily: cofilin

Query Match

Best Local Similarity 14.1%; Score 103.5; DB 2; Length 133;

Best Local Similarity 26.4%; Pred. No. 0.015;

Matches 33; Conservative 30; Mismatches 41; Indels 21; Gaps 6;

QY 13 ELTEKLRKFRKFTDAAIIMKYDKDRQVYLEEFQNI-----SPEELKMELEPERQ 66

Db 13 ELKER-KFR-----SIYKIDNMQVIEKHKKMGERSQSYEEFANSLPADEC 63

QY 67 RFVVSYSKYVHDDGRVSPPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAEITKVFPIRTT 126

Db 64 RYALIDIEFVPEKRI-----CFIAMSPTAKMKKMIYSSTKDRFKRELDGIQV-EFHAT 118

QY 127 DDLTE 131

Db 119 -DLTD 122

Search completed: September 23, 2003, 15:11:51
Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 23, 2003, 14:58:43 : Search time 24 Seconds
(without alignments)
278.241 Million cell updates/sec

Title: US-10-004-832-2

Perfect score: 735

Sequence: 1 MSDSLVCEVPELLEKLRK.....IRTDDELLEAMLOEKLSFRR 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	735	100.0	142	1	GLMG_HUMAN
2	617	83.9	141	1	GLMB_HUMAN
3	611	83.1	141	1	GLMB_RAT
4	111.5	15.2	140	1	ADPF_ARATH
5	109	14.8	139	1	ADPF_LILLO
6	108	14.7	139	1	ADPF_ARATH
7	105	14.3	139	1	ADPF_ARATH
8	104	14.1	139	1	ADPF_ARATH
9	103	14.0	139	1	ADPF_PETRY
10	100.5	13.7	143	1	ADPF_PETRY
11	97.5	13.3	137	1	ACTP_ACACA
12	95	12.9	137	1	ADPF_ARATH
13	93	12.7	146	1	ADPF_ARATH
14	92.5	12.6	137	1	CORF_SCHPO
15	91.5	12.4	137	1	CORF_DICDI
16	91	12.4	126	1	ADPF_BRANA
17	90.5	12.3	332	1	TWFL_YEAST
18	85.5	11.6	139	1	ADPF_MAIZE
19	84	11.4	143	1	ADPF_ARATH
20	82.5	11.2	166	1	CORF_HUMAN
21	82.5	11.2	166	1	CORF_MOUSE
22	82.5	11.2	166	1	CORF_MOUSE
23	80.5	11.0	166	1	CORF_MOUSE
24	80.5	11.0	427	1	RMOC_CHLIR
25	80.5	11.0	520	1	RECNA_AQUAE
26	79.5	10.8	168	1	CORF_XENLA
27	79	10.7	165	1	DEST_CHICK
28	78.5	10.7	166	1	CORF_HUMAN
29	78.5	10.7	166	1	CORF_MOUSE
30	78.5	10.7	166	1	CORF_MOUSE
31	77.5	10.5	166	1	CORF_MOUSE
32	77	10.5	161	1	MPH6_MOUSE
33	76	10.3	139	1	ADPF_MAIZE

34	76	10.3	165	1	DEST_MOUSE
35	76	10.3	875	1	DPO1_SULAC
36	75.5	10.3	165	1	DEST_HUMAN
37	75.5	10.3	168	1	CORF_XENLA
38	73.5	10.0	425	1	RMOC_CHLIR
39	73	9.9	559	1	INXA_CAEEL
40	73	9.9	624	1	HTPE_CLOAB
41	72	9.8	363	1	YGDE_HAEIN
42	71.5	9.7	366	1	ARGD_PYRPU
43	71	9.7	143	1	CORF_YEAST
44	71	9.7	345	1	HRCA_LISIN
45	71	9.7	345	1	HRCA_LISMO

ALIGNMENTS

RESULT 1	
GLMG_HUMAN	
ID	GLMG_HUMAN
AC	060234; STANDARD; PRT; 142 AA.
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	Glia maturation factor gamma (GMF-gamma).
GN	GMF.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Brain;
RX	MEDLINE=9820713; PubMed=9545571;
RA	Asai K., Fujita K., Yamamoto M., Hotta T., Morikawa M., Kokubo M.,
RA	Moriyama A., Kato T.;
RT	"Isolation of novel human CDNA (hGMF-gamma) homologous to Gila
RT	maturation factor-beta gene.";
RL	Biophys. Acta 1396:242-244(1998).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Blood;
RX	MEDLINE=98318631; PubMed=9653160;
RA	Mao M., Fu G., Wu J.-S., Zhang Q.-H., Zhou J., Kan L.-X., Huang Q.-H.,
RA	He K.-L., Gu B.-W., Han Z.-G., Shen Y., Gu J., Yu Y.-P., Xu S.-H.,
RA	Wang Y.-X., Chen S.-J., Chen Z.;
RT	"Identification of genes expressed in human CD34(+) hematopoietic
RT	stem/progenitor cells by expressed sequence tags and efficient full-
RT	length cDNA cloning.";
RL	Proc. Natl. Acad. Sci. U.S.A. 95:8175-8180(1998).
RN	[3]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20009844; PubMed=10541589;
RA	Peters N., Smith J.S., Tachibana I., Lee H.K., Pohl U., Portier B.P.,
RA	Louis D.N., Jenkins R.B.;
RT	"The human glia maturation factor-gamma gene: genomic structure and
RT	mutation analysis in gliomas with chromosome 19q loss.";
RL	Neurogenetics 2:163-166(1999).
CC	-!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LUNG, HEART, AND
CC	PLACENTA.
CC	-!- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY. GMF
CC	SUBFAMILY.
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CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC	or send an email to license@sib-sib.ch).
DR	EMBL; AB001993; BAA25572.1; -
DR	EMBL; AF038956; AAC39870.1; -

DR EMBL: AF108027; AAD27807.1; -.
 DR EMBL: AF108022; AAD27807.1; JOINED.
 DR EMBL: AF108023; AAD27807.1; JOINED.
 DR EMBL: AF108024; AAD27807.1; JOINED.
 DR EMBL: AF108025; AAD27807.1; JOINED.
 DR EMBL: AF108026; AAD27807.1; JOINED.
 DR Genew: HGNC:4374; GMFB.
 DR MIM: 604104; -.
 DR GO: GO:0008047; F:enzyme activator activity; TAS.
 DR GO: GO:0004860; F:protein kinase inhibitor activity; TAS.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR InterPro: IPR002108; Actbind_coflin.
 DR Pfam: PF00241; cofilin_Adf; 1.
 DR SMART: SM00102; ADF; 1.
 DR Growth factor.
 KW SEQUENCE 142 AA; 16801 MW; DB64BD8DE4F88170 CRC64;

Query Match 100.0%; Score 735; DB 1; Length 142;
 Best Local Similarity 100.0%; Pred. No. 3.2e-60;
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSDSLVCEVDEPLETEKLRFRFRKRETDNAIIMKVDKRDQNVYLEEFONISPEELKME 60
 DB 1 MSDSLVCEVDEPLETEKLRFRFRKRETDNAIIMKVDKRDQNVYLEEFONISPEELKME 60
 OY 61 LPERQPREVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTALTKV 120
 DB 61 LPERQPREVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTALTKV 120
 OY 121 FEIRTDLTTEAMLOEKISFFR 142
 DB 121 FEIRTDLTTEAMLOEKISFFR 142

RESULT 2

GLMB_HUMAN

ID GLMB_HUMAN STANDARD; PRT; 141 AA.

AC P17774;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-AUG-1990 (Rel. 15, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Gila maturation factor beta (GMF-beta).

GN GMFB.

OS Homo sapiens (Human), and

OS Bos taurus (Bovine).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606, 9913;

RN [1]

RP SEQUENCE FROM N.A.

RC SPECIES=Human;

RX MEDLINE=91303115; PubMed=1712830;

RA Kaplan R., Zaher A., Jaye M., Lim R.;

RT "Molecular cloning and expression of biologically active human gila

RL maturation factor-beta.";

RL J. Neurochem. 57:483-490(1991).

RN [2]

RP SEQUENCE FROM N.A.

RC SPECIES=Human; TISSUE=Brain;

RL Saito T., Tanaka N., Toyomasu T.;

RN Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE.

RC SPECIES=Bovine; PubMed=2196564;

RA Lim R., Zaher A., Lane W.S.;

RT "Complete amino acid sequence of bovine gila maturation factor beta.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:5233-5237(1990).

RN [4]

RP PHOSPHORYLATION.

RC SPECIES=Human;

RX MEDLINE=93321959; PubMed=7598724;

RA Lim R., Zaher A.;

2

RT "phorbol ester stimulates rapid intracellular phosphorylation of gila
 maturation factor.";
 RL Biochem. Biophys. Res. Commun. 211:928-934(1995).
 CC -1- FUNCTION: THIS PROTEIN CAUSES DIFFERENTIATION OF BRAIN CELLS,
 STIMULATION OF NEURAL REGENERATION, AND INHIBITION OF
 CC PROLIFERATION OF TUMOR CELLS.
 CC -1- PTM: PHOSPHORYLATED; STIMULATED BY PHORBOL ESTER.
 CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY. GMF
 CC SUBFAMILY.
 CC
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 DR EMBL: M86492; AA58614.1; -.
 DR EMBL: AB001106; BAA19232.1; -.
 DR PIR: A3102; JDBOB.
 DR PIR: PT0410; PT0410.
 DR Genew: HGNC:4373; GMFB.
 DR MIM: 601713; -.
 DR GO: GO:0008047; F:enzyme activator activity; TAS.
 DR GO: GO:0004860; F:protein kinase inhibitor activity; TAS.
 DR GO: GO:0004871; F:signal transducer activity; TAS.
 DR GO: GO:0007399; P:neurogenesis; TAS.
 DR GO: GO:0006468; P:protein amino acid phosphorylation; TAS.
 DR GO: GO:0007165; P:signal transduction; TAS.
 DR InterPro: IPR002108; Actbind_coflin.
 DR Pfam: PF00241; cofilin_Adf; 1.
 DR SMART: SM00102; ADF; 1.
 DR Growth factor; Acetylation; Phosphorylation.
 FT INT_MET 0
 FT MOD_RES 1
 FT SEQUENCE 141 AA; 16582 MW; EE1DA4FE200E2F370 CRC64;

Query Match 83.9%; Score 617; DB 1; Length 141;
 Best Local Similarity 82.1%; Pred. No. 1.7e-49;
 Matches 115; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

OY 2 SDSLVCEVDEPLETEKLRFRFRKRETDNAIIMKVDKRDQNVYLEEFONISPEELKME 61
 DB 1 SESLVCDVADIEDLEKLRFRFRKRETDNAIIMKVDKRDQNVYLEEFONISPEELKME 60
 OY 62 PERQPREVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTALTKV 121
 DB 61 PERQPREVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTALTKV 120
 OY 122 EIRTDLTTEAMLOEKISFF 141
 DB 121 EIRTDLTTEAMLOEKISFF 140

RESULT 3

GLMB_RAT

ID GLMB_RAT STANDARD; PRT; 141 AA.

AC O63228;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Gila maturation factor beta (GMF-beta).

GN GMFB.

OS Rattus norvegicus (Rat).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=93171924; PubMed=8436977;

RA Zaher A., Fink B.D., Lim R.;

RT "Expression of gila maturation factor beta mRNA and protein in rat


```

RT  organs and cells."
RL  J. Neurochem. 60:914-920(1993).
CC  -1- FUNCTION: THIS PROTEIN CAUSES DIFFERENTIATION OF BRAIN CELLS,
CC  STIMULATION OF NEURAL REGENERATION, AND INHIBITION OF
CC  PROLIFERATION OF TUMOR CELLS (BY SIMILARITY).
CC  -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY. GME
CC  SUBFAMILY.
CC  -----
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CC  -----
DR  EMBL; 211558; CAA7650.1; -.
DR  PIR; S22149; S22149.
DR  InterPro; IPR002108; Actbind_cofln.
DR  Pfam; PF00241; coflin_ADF; 1.
DR  SMART; SM00102; ADF; 1.
DR  Growth factor; Acetylation.
FT  INIT_MET 0
FT  MOD_RES 1
FT  SEQUENCE 141 AA; 16605 MW; 825B8DF33A5C703 CRC64;
SQ
Query Match 83.1%; Score 611; DB 1; Length 141;
Best Local Similarity 80.7%; Pred. No. 6,1e-49;
Matches 113; Conservative 16; Mismatches 11; Indels 0; Gaps 0;
QY 2 SDSLVCVCEVPELTERKLRFRKRTDNNAIIMKVDKRDQVYVLEEFQNISPELKMEL 61
   1:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:
DB 1 SESLVYCDVAEDLVETLRKFRKRNHNAIIMKIDKRLVLDLEEGVSPDELKDEL 60
QY 62 PERQPRFVYVSYKYVHDDGRVSPVLCFIFSSPVGCKPEQOMYAGSKNKLVTQALTYKF 121
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 PERQPRFVYVSYKYVHDDGRVSPVLCFIFSSPVGCKPEQOMYAGSKNKLVTQALTYKF 120
QY 122 ETRTDDTLTEANLQEKLSFF 141
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 121 ETRTDDTLTEANLQEKLSFF 140
RESULT 4
ADFX ARATH STANDARD; PRT; 140 AA.
AC Q9L081;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Actin-depolymerizing factor like At1g01750 (ADF-like).
GN AT1G01750 OR T1N6.16.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21016719; PubMed=1130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Cressy T.H., Dewar K.,
RA Dunn P., Egu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Malt R., Maritali A.,
RA Millschetter J., Miranda M., Nguyen M., Nieman W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

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RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tansburga G., Tortum M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana."
RL Nature 408:816-820(2000).
CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERES ACTIN FILAMENTS
CC (F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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DR  EMBL; AC009273; AAF78408.1; -.
DR  PIR; A86149; A86149.
DR  HSSP; Q39250; 1F7S.
DR  InterPro; IPR002108; Actbind_cofln.
DR  Pfam; PF00241; coflin_ADF; 1.
DR  ProDom; PD002129; Actbind_cofln; 1.
DR  SMART; SM00102; ADF; 1.
DR  PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
KW ACTin-binding; Multigene family.
FT DOMAIN 92
FT SEQUENCE 140 AA; 16341 MW; B9845FE24B637859 CRC64;
SQ
Query Match 15.2%; Score 111.5; DB 1; Length 140;
Best Local Similarity 28.1%; Pred. No. 0.0017;
Matches 34; Conservative 23; Mismatches 43; Indels 21; Gaps 5;
QY 13 ELTERKLRFRKRTDNNAIIMKVDKRDQVYVLEEFQNISPELKMELPEROP 66
   |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
DB 20 ELKAR-RNRF-----IVRKIDKKAQVWMDLGNPELY-----EDFRSRSPEDBC 65
QY 67 RFVYVSYKYVHDDGRVSPVLCFIFSSPVGCKPEQOMYAGSKNKLVTQALTYKFIRTT 126
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
DB 66 RFVYVSYKYVHDDGRVSPVLCFIFSSPVGCKPEQOMYAGSKNKLVTQALTYKFIRTT 124
QY 127 D 127
DB 125 D 125
RESULT 5
ADFX LILLO STANDARD; PRT; 139 AA.
ID ADF_LILLO
AC P30175;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Actin-depolymerizing factor (ADF).
OS Lilium longiflorum (Trumpet lily).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
OC Lilium.
OX NCBI_TaxID=4690;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nellie white; TISSUE=Pollen;
RA MEDLINE=93144690; PubMed=8425049;
RA Kim S.-R., Kim Y., An G.;
RT "Molecular cloning and characterization of anther-preferential cDNA
RT encoding a putative actin-depolymerizing factor."
RL Plant Mol. Biol. 21:39-45(1993).
CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERES ACTIN FILAMENTS
CC (F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: PREFERENTIALLY IN MATURE ANTHER.
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.

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DR      EMBL; Z1A110; CA78483.1; -.
DR      PIR; S30935; S30935.
DR      HSSP; Q39250; IETS.
DR      InterPro; IPRO02108; Actbind_cofin.
DR      Pfam; PF00241; cofilin_ADF.1.
DR      Prodom; PD002129; Actbind_cofin; 1.
DR      SMART; SM00102; ADF.1.
DR      PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
KM      Actin-binding.
FT      DOMAIN          92      111      ACTIN-BINDING (POTENTIAL).
SO      SEQUENCE       139 AA; 16226 MW; 0B45CC67136F1EA9 CRC64;

Query Match              14.8%; Score 109; DB 1; Length 139;
Best Local Similarity    27.6%; Pred. NO. 0.0029;
Matches   37; Conservative 26; Mismatches 55; Indels 16; Gaps 4;

OY      1 MSDSLVCEVDPELTEKL-----RFRFKETDMAIIMKYDKRDROMVYLEEERQ-NIS 53
DB      1 MANSSGCAWVDECKLFMELKAKRNRF-----IVFKIEKVQQVTVERLGQPRES 52
OY      54 PEELKMELEPRQPFVVYSYKYVDDGKVSIFLCFISSPYGCAPEDQOMTAGSKNRLVQ 113
DB      53 YDDTECPPEPCNECRAYAFDFPDVIDENCQKSIFETISWSPTSRVRSKMLASTKDREKR 112
OY      114 TAEITKVFIERITTD 127
DB      113 ELDTGIQV-ELQATD 125

RESULT 6
ADFL_ARATH ADFL_ARATH STANDARD: PRT; 139 AA.
AC Q39250:
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Actin-depolymerizing factor 1 (ADF-1) (AtADF1).
GN ADF1 OR ATG3646010 OR F16L2_220.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RA Staiger C.J., Ashworth S.L.;
RT "Actin depolymerizing factor from Arabidopsis thaliana severs
RT polymers and binds to monomers in a pH-dependent manner.";
RL Submitted (FEB-1996) to the EMBL/Genbank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A. AND CHARACTERIZATION.
RP STRAIN=cv. Columbia;
RX MEDLINE=21307188; PubMed=11414611;
RA Dong C.-H., Kost B., Xia G., Chua N.-H.;
RT "Molecular identification and characterization of the Arabidopsis
RT AtADF1, AtADF5 and AtADF6 genes."
RL Plant Mol. Biol. 45:517-527(2001).
RN [3]
RP SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger H., Perez-Alonso M., Obermaier B.,
RA Fatemoun B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
```

RESULT 7

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RA DelSigne M., Boutry M., Griwell L.A., Maché R., Putgondemach P.,  
RA De Simone V., Choisne N., Artiguenave F., Robert C., Brotlier P.,  
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quétier F.,  
RA Schuber E., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,  
RA Wunderlich E., Drzcone H., Erfle H., Jordan N., Bangert S.,  
RA Wielandmann R., Kranz H., Voss H., Holland R., Brandt P., Nakakura G.,  
RA Vezi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,  
RA Conrad A., Hornschke K., Kaiser G., Loehner T.-H., Nordfeld G.,  
RA Reichelt J., Schwarzer M., Schoen O., Barques M., Terol J., Clement J.,  
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Ducheman D.,  
RA Cooke R., Landie M., Berger-Liauzo C., Furnelle B., Masny D.,  
RA De Haan M., Maare A.C., Alcaraz J.-P., Cottet A., Casacubeta E.,  
RA Monfort A., Argilhou A., Flores M., Ligouri R., Vitale P.,  
RA Mannheim G., Haase D., Schoof H., Rudd S., Zaccaria P., Meves H.-W.,  
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon I.J., Jenkins J.,  
RA Rooney T., Rizzo M., Walts A., Utechtack T., Fujii C.Y., Shea T.P.,  
RA Creasy T.H., Haas B., Maitl R., Wu D., Peterson J., Van Aken S.,  
RA Pal G., Millschler J., Sellers P., Gill J.E., Feldblum T.V.,  
RA Preuss D., Lin X., Niemman W.C., Salzberg S.L., White O., Venter J.C.,  
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E.,  
RA Sasamoto S., Kimura T., Ideawa K., Kawashima K., Kishida Y.,  
RA Kiyoikawa C., Kohara M., Matsuno M., Matsumoto A., Muraki A.,  
RA Nakayama S., Nakasaki N., Shino S., Takeuchi C., Wada T.,  
RA Wakanahe A., Yamada M., Yasuda M., Tabata S.;  
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis  
RT thaliana.";  
RL Nature 408:820-822(2000).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=20481864; PubMed=11025546.  
SA Bowman G.D., Noedelmaun I.M., Hong Y., Chua N.H., Lindberg U.,  
RA Schutt C.E.;  
RT "A comparative structural analysis of the ADF/cofilin family.";  
RL Proteins 41:374-384(2000).  
CC -I- FUNCTION: ACTIN-DOPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS  
    (F-ACTIN) AND BINDS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.  
CC -----  
CC -I- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.  
CC -----  
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CC CC  
DR EMBL; U49398; AAC03696.1; -  
DR EMBL; AF102173; AAC72407.1; -  
DR EMBL; AL162459; CAB88325.1; -  
DR PDB; 1PT5; 15-NOV-00  
DR InterPro; IPRO02108; Actbind_coflin.  
DR Pfam; PF00241; cofilin_ADF.1.  
DR ProDom; PD002129; Actbind_coflin; 1.  
DR SMART; SM00102; ADF; 1.  
DR POSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.  
KW Actin-binding; Multigene family; 3D-structure.  
FT DOMAIN 92      111     ACTIN-BINDING (POTENTIAL).  
SQ SEQUENCE   139 AA;  16112 MW;  E3429B0FE23A94AF CRC64;
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Query Match 14.7%; Score 108; DB 1; Length 139;
Best Local Similarity 27.7%; Pred. NO. 0.0035;
Matches 31; Conservative 26; Mismatches 53; Indels 2; Gaps 2;

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Oy 17 KLKRFRRKETDNAAITMKVDQOMVYLEEFPONISPELKMLNEDEPRQFRFYYSKY 75  
    ||| : : : : | : : : : | : : : : | : : : : | : : : : | : : : :  
Db 15 KLRLELRAKKTTHREIFYIKIEKKOVVEVGPIPTYEFAPCLADECRVAIDYDF 74  
  
Oy 76 VHDDGRVSYPICFIFFSPGCKPFPOGMVYAGSKRLVTQATLVTFVFETRTD 127  
    | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 75 VTAEKCKSKTIFFIAKCPDLAKAVASKMIYASKSQRDKFRELDGIQV-EIQATD 125
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ADPF4_ARATH          STANDARD:          PRT:      139 AA.
ID  ADPF3_ARATH
AC  09ZSK3: 09FEJ7;
DT  28-FEB-2003 (Rel. 41, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  28-FEB-2003 (Rel. 41, Last annotation update)
DE  Actin-depolymerizing factor 4 (ADF-4) (AtADF4).
GN  ADF4 OR AT5G59890 OR MNM10.13.
OS  Arabidopsis thaliana (Mouse-ear cress).
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC  eustosids II; Brassicales; Brassicaceae; Arabidopsids.
OX  NCBI_TaxID=3702;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=cv. Columbia;
RX  MEDLINE=21307188; Pubmed=11414611;
RA  Dong C.-H., Kost B., Xia G., Chua N.-H.;
RT  "Molecular identification and characterization of the Arabidopsis
RT  AtADF1, AtADF5 and AtADF6 genes.";
RL  Plant Mol. Biol. 45:517-527(2001).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=cv. Columbia;
RX  MEDLINE=99087489; Pubmed=9872454;
RA  Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
RA  Tabata S.;
RT  "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
RT  Sequence features of the regions of 1,013,767 bp covered by sixteen
RT  physically assigned pl and TAC clones."
RL  DNA Res. 5:297-308(1998).
-1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS
-1- (F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
-----
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@sib-sib.ch).
-----
DR  EMBL: AF102822; AAD09110.1; -
DR  EMBL: AB015475; BAB08357.1; -
DR  HSSP: Q39250.1;7S.
DR  InterPro: IPR002108; Actbind_cofln.
DR  Pfam: PF00241; coflin_ADF.1.
DR  ProDom: PD002129; Actbind_cofln.1.
DR  SMART: SM00102; ADF.1.
DR  ProSite: PS00325; ACTIN-DEPOLYMERIZING; 1.
KW  Actin-binding; Multigene family.
FT  DOMAIN 92 111
FT  CONFLICT 117 111 ACTIN-BINDING (POTENTIAL).
FT  CONFLICT 117 117 I -> R (IN REF. 1).
FT  CONFLICT 134 134 L -> W (IN REF. 1).
SQ  SEQUENCE 139 AA; 16034 MW; 57E95F557FE42P863 CRC64;

Query Match 14.3%; Score 105; DB 1; Length 139;
Best Local Similarity 25.0%; Pred. No. 0.0066;
Matches 28; Conservative 30; Mismatches 52; Indels 2; Gaps 2;

17 KLRKFRFEKEDNAAIIMVKDKQMVNLEEEFQNI-SPEELKMELEPEROPFVYVSYKY 75
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db KLRLELKAKRTHRFIVYIKIEKKQYIVKVEVGEIDILTYEDFPASLPDDECKRAYIYDDF 74

QY 76 VHDGGRVSYPLCFIFSSPVGCKPEQOMYAGSKNKLVTQAEITKVEFIRTTD 127
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 75 VTAENCCKSKITFFIAMCPDAKVYKSKMIATYASCKDFKRELDTGIQV-ELQARD 125

RESULT 8
ADPF3_ARATH          STANDARD:          PRT:      139 AA.
ID  ADPF3_ARATH

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AC 09ZSK4; 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Actin-depolymerizing factor 3 (ADF 3) (AtADF3).
GN ADF3 OR AT5G59880 OR MN10.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eustosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21307188; PubMed=11414611.
RA Dong C.-H., Kost B., Xia G., Chua N.-H.,
RT "Molecular identification and characterization of the Arabidopsis
RL AtADF1, AtADF5 and AtADF6 genes."
RN Plant Mol. Biol. 45:517-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=99087489; PubMed=9872454;
RA Nakamura Y., Sato S., Asamizu E., Kaneko T., Kotani H., Miyajima N.,
RT Tabata S.;
RN "Structural analysis of Arabidopsis thaliana chromosome 5. VII.
RT Sequence features of the regions of 1,013,767 bp covered by sixteen
RL physically assigned P1 and TAC clones."
RN DNA Res. 5:297-308(1998).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "RIKEN Arabidopsis full length cDNA clones (RACLs) sequenced by the
RL SSCP consortium (Salk/Stanford/PfGEC)."
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS
CC (F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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CC -----
DR EMBL; AF102821; AAD09109.1; -
DR EMBL; AB015475; BAB08356.1; -
DR EMBL; AF360169; AAK25879.1; -
DR HSSP; Q39250; IPTS.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; cofilin_ADF.1.
DR ProDom; PD002129; Actbind_cofin.1.
DR SMART; SM00102; ADF.1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING.1.
DR Actin-binding; Multigene family.
FT DOMAIN 92 111 ACTIN-BINDING (POTENTIAL).
FT SEQUENCE 139 AA; 15922 MW; D3325AAV7IDDD102E CRC64;
SO

Query Match 14.1%; Score 104; DB 1; Length 139;
Best Local Similarity 24.1%; Pred. No. 0.0081;
Matches 27; Conservative 33; Mismatches 50; Indels 2; Gaps 2;
QY 17 KLRFRPRKKTDNAAILMKYDKDQMVLLLEEFQ-NISPEELKMLPEQRPVYVSYKY 75
DB 15 KLRKEMELKTRKTRHFIYIKIELOKOYIVKIGEPGQTHEDLASLPADRCRYAIFDEDF 74
QY 76 VHDGGRSYPLCFIFSSPVGCGKPRQDQMMYAGSKNRLLVQTAALTIVFEKRTD 127
DB 75 VSSGSGVPSRSLTFEVAWSPDARVBSKMIYAKSKDFKRELDGIVQ-ELQAD 125

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RESULT 9
ADFL_PETHY STANDARD; PRT; 139 AA.
AC Q9FV12;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
GN ADPL
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20534787; PubMed=11080583;
RA Mun J.-H., Yu H.-J., Lee H.S., Kwon Y.M., Lee J.S., Lee I., Kim S.-G.;
RT "Two closely related cDNAs encoding actin-depolymerizing factors of
petunia are mainly expressed in vegetative tissues."
RL Gene 257:167-176(2000).
CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS
CC (-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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CC -----
DR EMBL; AF183903; AACG16973.1; -.
DR HSSP; Q39250; 1F7S.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; cofilin_ADF; 1.
DR PRODOM; PD002129; Actbind_cofin; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
KW Actin-binding; Multigene family.
FT DOMAIN 92 111 ACTIN-BINDING (POTENTIAL).
FT SEQUENCE 139 AA; 16041 MW; 008073E2C6A28F0B CRC64;
SQ
Query Match 14.0%; Score 103; DB 1; Length 139;
Best Local Similarity 25.9%; Pred. No. 0.01;
Matches 29; Conservative 28; Mismatches 53; Indels 2; Gaps 2;
QY 17 KLRKFRPKETDAAIIMKYDKRQNVYLEEEFQ-NISPELKMELPERQPRFVVSXYK 75
Db 15 KLRLELAKRTHRFYIKIEKQYVVERIGEPTESYEDFAASLDPNECRVAVPDF 74
QY 76 VHDGGRSYPLCFIFSSPGVCKPEQOMMYAGSKNRVLQVTAELTVFEIRPTD 127
Db 75 VTAENCKSRIFLAWCPDTRAVRSKMIVASSKDRFRRELDGIQV-ELQACD 125
RESULT 10
ADFL_PETHY STANDARD; PRT; 143 AA.
AC Q9FV12;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
GN ADP2.
OS Petunia hybrida (Petunia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; solanales; Solanaceae; Petunia.
OX NCBI_TaxID=4102;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=20534787; PubMed=11080583;
RA Mun J.-H., Yu H.-J., Lee H.S., Kwon Y.M., Lee J.S., Lee I., Kim S.-G.;
RT "Two closely related cDNAs encoding actin-depolymerizing factors of
petunia are mainly expressed in vegetative tissues."
RL Gene 257:167-176(2000).
CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS
CC (-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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CC -----
DR EMBL; AF183904; AACG16974.1; -.
DR HSSP; Q39250; 1F7S.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; cofilin_ADF; 1.
DR PRINTS; PR00006; COFILIN.
DR PRODOM; PD002129; Actbind_cofin; 1.
DR SMART; SM00102; ADF; 1.
DR PROSITE; PS00325; ACTIN_DEPOLYMERIZING; 1.
KW Actin-binding; Multigene family.
FT DOMAIN 92 111 ACTIN-BINDING (POTENTIAL).
FT SEQUENCE 143 AA; 16510 MW; 408E035DDE61C05C CRC64;
SQ
Query Match 13.7%; Score 100.5; DB 1; Length 143;
Best Local Similarity 28.4%; Pred. No. 0.017;
Matches 33; Conservative 26; Mismatches 46; Indels 11; Gaps 4;
QY 13 ELTEKLKFRPKETDAAIIMKYDKRQNVYLEEEFQ-NISPELKMELPERQPRFVVS 71
Db 20 ELKAK-RPYRP-----IIYKIEKQEVVEKLEPESYEDFTAGLPADCRVAV 70
QY 72 SYRVHDDGRVSYPLCFIFSSPGVCKPEQOMMYAGSKNRVLQVTAELTVFEIRPTD 127
Db 71 DFDPMTEKNCKSRIFLAWCPDTRAVRSKMIVASSKDRFRRELDGIQV-ELQACD 125
RESULT 11
ACTP_ACACA STANDARD; PRT; 137 AA.
AC P37167;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
GN Actophorin.
OS Acanthamoeba castellanii (Acanthamoeba).
OC Eukaryota; Acanthamoebidae; Acanthamoeba.
OX NCBI_TaxID=5755;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 1-105, AND X-RAY CRYSTALLOGRAPHY.
RX MEDLINE=93363583; PubMed=8357799;
RA Oukir S., Maciver S.K., Ampe C., Doberstein S.K., Kalsner D.A.,
RA van Damme J., Vandekerckhove J., Pollard T.D.;
RT "Primary structure of and studies on Acanthamoeba actophorin."
RL Biochemistry 32:8525-8533(1993).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX MEDLINE=97290450; PubMed=9145107;
RA Leonard S.A., Gittis A.G., Petrella E.C., Pollard T.D., Latman E.E.;
RT "Crystal structure of the actin-binding protein actophorin from
RT Acanthamoeba."
RL Natl. Struct. Biol. 4:369-373(1997).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS).
RX MEDLINE=98411306; PubMed=9737968;
RA Blanchon L., Pollard T.D.;
RT "Interaction of actin monomers with Acanthamoeba actophorin

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RT (ADF/cofilin) and profilin."
RL J. Biol. Chem. 273:25106-25111(1998).
CC -1- FUNCTION: FORMS A ONE TO ONE COMPLEX WITH MONOMERIC ACTIN. CAN
CC REGULATE THE POOL AVAILABLE FOR POLYMERIZATION. SEVERS ACTIN
CC FILAMENTS IN A DOSE-DEPENDENT MANNER.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
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CC -----
CC EMBL: M9361; AAA02909.1; -.
CC PDB: 1AHQ; 04-SEP-97.
CC DR InterPro: IPR002108; Actbind_cofiln.
CC pfam: PF00241; cofilin_ADF. 1.
CC PRINTS: PR00006; COFILIN.
CC PRODOM: PD002129; Actbind_cofiln. 1.
CC SMART: SM00102; ADF. 1.
CC DR PROSITE: PS00325; ACTIN_DEPOLYMERIZING. 1.
CC KW Actin-binding; 3D-structure.
CC FT INIT MET 0 0
CC FT MOD_RES 1 1 BLOCKED.
CC FT DOMAIN 86 105 ACTIN-BINDING (POTENTIAL).
CC FT STRAND 4 5
CC FT HELIX 7 19
CC FT STRAND 24 29
CC FT TURN 31 32
CC FT STRAND 35 41
CC FT TURN 44 45
CC FT HELIX 48 52
CC FT TURN 53 54
CC FT TURN 57 58
CC FT STRAND 61 71
CC FT TURN 72 73
CC FT STRAND 74 84
CC FT TURN 87 88
CC FT HELIX 91 107
CC FT TURN 109 110
CC FT STRAND 113 117
CC FT TURN 120 123
CC FT HELIX 125 132
CC FT TURN 133 133
CC SQ SEQUENCE 137 AA; 15422 MW; D16030ABA4EF6347B CRC64;

Query Match 13.3%; Score 97.5; DB 1; Length 137;
Best Local Similarity 25.7%; Pred. No. 0.031;
Matches 28; Conservative 30; Mismatches 46; Indels 5; Gaps 4;

QY 32 IMKVDKDKOMVYLEE-EFQNISPELKMELPERQPRFVYVSYKYVHDGRSYDLCFF 90
DB 25 VFKKMASTVEYVEHVEGPNATYEDFSQDLPERCRAIFYEFQVGGGRN-KITFL 83
QY 91 SSPVCCPEQOMMYAGSKNRNLVOTAELEKVFETRTD--DLTEAWLOEK 137
DB 84 WAPDSAPIKSKMWTSTKDSIKKLVGIQV-EVQATDAEISEDAVSR 131

RESULT 12
ADF2_ARATH STANDARD: PRT; 137 AA.
AC Q39251; O9LZT2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Actin-depolymerizing factor 2 (ADF-2) (AtADF2).
GN ADF2 OR AT3G46000 OR F16L2_210.

```

```

OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RA Staiger C.J., Ashworth S.L.;
RT "Actin depolymerizing factor from Arabidopsis thaliana severs
RT polymers and binds to monomers in a pH-dependent manner."
RL Submitted (FEB-1996) to the EMBL/Genbank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseid M.,
RA Faltmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaler B.,
RA Delseny M., Boutry M., Griveil L.A., Mache R., Puldomenech P.,
RA De Simone V., Choisme N., Artiguenave F., Robert C., Brotier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erile H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordstiek G.,
RA Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwelder B., Duchemin D.,
RA Cooke R., Laude M., Berger-Liauro C., Purnelle B., Masy D.,
RA de Haan M., Maiese A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argirou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins P.,
RA Rooney T., Rizzo M., Wals A., Uterback T., Fujii C.Y., Shea T.P.,
RA Creeasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S.,
RA Pai G., Millscher J., Sellers P., Gill J.E., Feldlyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneo T., Nakamura Y., Sato S., Kato T., Asamizu E.,
RA Sasamoto S., Kimura T., Idegawa K., Kawashina K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shindo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana."
RL Nature 408:820-822(2000).
CC -1- FUNCTION: ACTIN-DEPOLYMERIZING PROTEIN. SEVERS ACTIN FILAMENTS
CC (F-ACTIN) AND BINDS TO ACTIN MONOMERS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U48939; AAB03697.1; -.
CC DR EMBL: AL162459; CAB82824.1; ALT_INIT.
CC DR HSSP: Q39250; 1F7S.
CC DR InterPro: IPR002108; Actbind_cofiln.
CC pfam: PF00241; cofilin_ADF. 1.
CC DR PRODOM: PD002129; Actbind_cofiln. 1.
CC DR SMART: SM00102; ADF. 1.
CC DR PROSITE: PS00325; ACTIN_DEPOLYMERIZING. 1.
CC KW Actin-binding; Multigene family.
CC FT DOMAIN 90 109 ACTIN-BINDING (POTENTIAL).
CC SQ SEQUENCE 137 AA; 15745 MW; BE28582817394046 CRC64;

Query Match 12.9%; Score 95; DB 1; Length 137;
Best Local Similarity 25.2%; Pred. No. 0.053;
Matches 28; Conservative 26; Mismatches 55; Indels 2; Gaps 2;

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CC BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE
CC MAJOR COMPONENT OF INTRANUCLEAR AND CYTOPLASMIC ACTIN RODS
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTRANUCLEAR AND CYTOPLASMIC
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: D89939; BAAL4039.1; -.
CC EMBL: Z98600; CAB11258.1; -.
CC PIR: T43245; T43245.
CC HSSP: Q03048; ICOF.
CC GenedB, Spombe: SPAC20G4.06c; -.
CC InterPro: IPR002108; Actbind_cofilin.
CC Pfam: PF00241; cofilin_ADF; 1.
CC PRINTS: PR00006; COFILIN.
CC ProDom: PD002129; Actbind_cofilin; 1.
CC SMART: SM00102; ADF; 1.
CC PROSITE: PS00325; ACTIN DEPOLYMERIZING; 1.
CC ACTIN-binding; Cytoskeleton.
CC FT DOMAIN 88 107
CC SEQUENCE 137 AA; 15620 MW; ECC6D354C959E04 CRC64;

Query Match
Best Local Similarity 12.6%; Score 92.5; DB 1; Length 137;
Matches 26; Conservative 33; Mismatches 50; Indels 13; Gaps 3;

OY 9 EVDPELTKLRFRFKETDNNALIMKYDKDQWVLEEFQNISPEELKMLPEROPRF 68
DB 7 KVSPECLAFQELKTKGSL--RYVVFKNMDKTEIVEKSKTDKDFLDLPKDDRY 64
OY 69 VVYSKRYVHDGRVSYPLCFITFSFVGCKPEQOMKTAGSKNRL-----VQTAELT 118
DB 65 AIYDFEFLNGEG-VNKKIIFISWSPDVAPIKSKMYSSKDTLLRAFTGIGTDIQTDF 123
OY 119 KV 120
DB 124 EV 125

RESULT 15
COFI_DICDI
ID COFI_DICDI STANDARD; PRT; 137 AA.
AC P54706;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Cofilin.
GN (COFA OR COFI) AND (COFB OR COF2).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX2;
RX MEDLINE=95526267; PubMed=7738034;
RA Aizawa H., Sutoh K., Tsubuki S., Kawashima S., Ishii A., Yahara I.,
RT "Identification, characterization, and intracellular distribution of
RT cofilin in Dictyostelium discoideum.",
RL J. Biol. Chem. 270:10923-10932(1995).
CC -1- FUNCTION: CONTROLS REVERSIBLY ACTIN POLYMERIZATION AND
CC DEPOLYMERIZATION IN A PH-SENSITIVE MANNER. IT HAS THE ABILITY TO
CC BIND G- AND F-ACTIN IN A 1:1 RATIO OF COFILIN TO ACTIN. IT IS THE
CC MAJOR COMPONENT OF INTRANUCLEAR AND CYTOPLASMIC ACTIN RODS
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTRANUCLEAR AND CYTOPLASMIC

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CC (BY SIMILARITY).
CC -1- MISCELLANEOUS: THERE ARE TWO GENES FOR COFILIN IN D.DISCOIDEUM,
CC THEY ENCODE FOR IDENTICAL PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE ACTIN-BINDING PROTEINS ADF FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: D37980; BA07198.1; -.
CC EMBL: D37981; BA07199.1; -.
CC HSSP: Q03048; ICOF.
CC SWISS-2DPAGE: P54706; DICTY.
CC DICTYDB: DD01059; COFA.
CC DICTYDB: DD01059; COFB.
CC InterPro: IPR002108; Actbind_cofilin.
CC Pfam: PF00241; cofilin_ADF; 1.
CC PRINTS: PR00006; COFILIN.
CC ProDom: PD002129; Actbind_cofilin; 1.
CC SMART: SM00102; ADF; 1.
CC PROSITE: PS00325; ACTIN DEPOLYMERIZING; 1.
CC Nuclear protein; Actin-binding; Cytoskeleton; Multigene family.
CC SEQUENCE 137 AA; 15224 MW; 0C0B057354F46F3 CRC64;

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Query Match
Best Local Similarity 12.4%; Score 91.5; DB 1; Length 137;
Matches 29; Conservative 26; Mismatches 49; Indels 5; Gaps 4;

OY 32 IIMKYDKDQWVLEEF-QNISPEELKMLPEROPRFVVSYKYVHDGRVSYPLCFIT 90
DB 27 IYRISDSKEIIVSTLPACGSFDEFKCLPENECRYVLDYQ-KEGAQSKICFVA 85
OY 91 SSPVCKRQEQOMMYGSKNRLVQTAELKVEIRFTD--DLTEAMLOEK 137
DB 86 WCPDTANIKRKMATSSKDSKLKACVGIQV-EIQGTDASEVNDSCFYER 133

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Search completed: September 23, 2003, 15:09:18
Job time : 25 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:05:44 : Search time 98 Seconds
(without alignments)
373.913 Million cell updates/sec

Title: US-10-004-832-2

Perfect score: 735

Sequence: 1 MSDSLVCEVDPDELTEKLRK.....IRTTDDLTEAMLQEKLSFRR 142

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SPREMBL_23:*
2: sp.archaea:*
3: sp.bacteria:*
4: sp.fungi:*
5: sp.human:*
6: sp.invertebrate:*
7: sp.mammal:*
8: sp.mhc:*
9: sp.organelle:*
10: sp.phage:*
11: sp.plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp.vertibrate:*
15: sp_unclassified:*
16: sp.virus:*
17: sp_bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	722	98.2	142	4	Q8TD26
2	695	94.6	142	11	Q9ERL7
3	622	84.6	154	4	Q9BS35
4	619	84.2	142	11	Q9ERL8
5	617	83.9	142	11	Q9COT3
6	600	81.6	142	13	Q9IBG6
7	379.5	51.6	138	5	Q9VJL6
8	373	50.7	138	5	Q9VJL6
9	261	35.5	145	5	Q8IAA5
10	185	25.2	145	5	Q8MSR7
11	175	23.8	141	3	Q13808
12	123.5	16.3	328	5	Q94399
13	119.5	16.3	333	5	Q20173
14	116.5	15.9	349	3	Q12156
15	113	15.4	252	4	Q8RCD3
16	113	15.4	350	4	Q12792

17	111.5	15.2	133	10	Q65277	Q65277 arabidopsis
18	111.5	15.2	140	10	Q8LC13	Q8LC13 arabidopsis
19	111	15.1	347	11	Q8BN77	Q8BN77 mus musculu
20	111	15.1	349	11	Q920P5	Q920P5 mus musculu
21	110	15.0	143	10	Q8SAG3	Q8SAG3 vltis vltif
22	110	15.0	347	11	Q9DCR8	Q9DCR8 mus musculu
23	109.5	14.9	343	5	Q9VEM9	Q9VEM9 drosophila
24	109	14.8	349	4	Q9Y3F5	Q9Y3F5 homo sapien
25	107	14.6	138	10	Q9XEN2	Q9XEN2 populus x c
26	106	14.4	129	10	Q9SW69	Q9SW69 malus domes
27	105	14.3	132	10	Q94A13	Q94A13 arabidopsis
28	104.5	14.2	156	6	Q8MIK3	Q8MIK3 bos taurus
29	104	14.1	145	10	Q8H9D5	Q8H9D5 solanum tub
30	103.5	14.1	133	10	Q9L2F3	Q9L2F3 arabidopsis
31	102.5	13.9	138	5	Q8T1J2	Q8T1J2 dictyostell
32	102.5	13.9	140	10	Q9M5Y4	Q9M5Y4 elaeis guin
33	102.5	13.9	145	10	Q9AY76	Q9AY76 oryza sativ
34	100.5	13.7	130	10	Q65603	Q65603 arabidopsis
35	99	13.5	153	10	Q9FWC0	Q9FWC0 oryza sativ
36	98.5	13.4	350	11	Q91YR1	Q91YR1 mus musculu
37	98.5	13.4	350	11	Q91YR1	Q91YR1 mus musculu
38	97.5	13.3	142	10	Q43655	Q43655 trifolium ae
39	96	13.1	139	10	Q8H2P8	Q8H2P8 oryza sativ
40	95.5	13.0	130	10	Q49606	Q49606 arabidopsis
41	95	12.9	146	10	Q8LCM6	Q8LCM6 arabidopsis
42	93.5	12.7	137	10	Q8H2B7	Q8H2B7 nicotiana t
43	92.5	12.6	130	10	Q9FHC4	Q9FHC4 arabidopsis
44	92.5	12.6	137	10	Q8LFR6	Q8LFR6 arabidopsis
45	91.5	12.4	137	10	Q8H2B6	Q8H2B6 nicotiana t

ALIGNMENTS

RESULT 1	
Q8TD26	PRELIMINARY: PRT: 142 AA.
AC Q8TD26:	
DT 01-JUN-2002 (TREMBLrel. 21, Created)	
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)	
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)	
DE Gila maturation factor gamma.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Asai K., Kawai Y., Inoue Y., Ueki T., Yamamoto M., Miura Y., Kato T.,	
RT "Homo sapiens Gila Maturation Factor gamma (GMEG) genomic DNA."	
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AB040440; BAB86591.1; -	
DR InterPro: IPR002108; Actbind_cofln.	
DR Pfam: PF00241; coflin_ADF.1.	
DR SMART: SM00102; ADF.1.	
DR SEQUENCE 142 AA; 16859 MW; DB64BD808BECD5A CRC64;	

Query Match 98.2%; Score 722; DB 4; Length 142;
Best Local Similarity 98.6%; Pred. No. 9.5e-63;
Matches 140; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY	1	MSDSLVCVDPDELTEKLRKFRKRETDNAALIMKVDKDRVMVLEEFQINISPELME	60
DB	1	MSDSLVCVDPDELTEKLRKFRKRETDNAALIMKVDKDRVMVLEEFQINISPELME	60
QY	61	LPERPFRVVSYSKYVHDGRVSPVLCIFSSPVCKREQQMMYAGSNRRVYQTAELTKV	120
DB	61	LPERPFRVVSYSKYVHDGRVSPVLCIFSSPVCKREQQMMYAGSNRRVYQTAELTKV	120
QY	121	FEIRTTDDLTEAMLQEKLSFRR	142
DB	121	FEIRTTDDLTEAMLQEKLSFRR	142

```
RESULT 2
O9ERL7 PRELIMINARY; PRT; 142 AA.
ID O9ERL7;
AC O9ERL7;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Gila maturation factor-gamma (0610039G16Rik protein) (2310057N07Rik
protein) (Gila maturation factor, gamma).
GN GMEG OR 0610039G16Rik OR 2310057N07Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss/TOPI OF1; TISSUE=Liver;
RC Bourgeois F., Guilmet F., Levacher B., Mas C., Simonneau M.J.;
RT "Identification and full-length cloning of GMEB, a putative
RT intracellular kinase regulator, expressed in proliferating
RT telencephalon stem cells."
RT Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo, Kidney, and Tongue;
RC MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamakata S.,
RA Saito T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Flaischman W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guenichon S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberees P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Welte C., Whitaker C., Wilmink L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RT Nature 409:685-690(2001).
[3]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (Jul-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF297221; AAC22804.1; -
DR EMBL: AK014214; BAB29210.1; -
DR EMBL: AK002834; BAB2392.1; -
DR EMBL: AK009967; BAB2617.1; -
DR EMBL: BC011468; AAH1148.1; -
DR MGD; MGI:1927135; Gmfg.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; cofillin_ADF.1.
DR SMART; SM00102; ADF.1.
SO SEQUENCE 142 AA; 16748 MW; 25367F2B49378710 CRC64;

Query Match 94.6%; Score 695; DB 11; Length 142;
Best Local Similarity 93.7%; Pred. No. 4,1e-60;
Matches 133; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
```

```
Oy 1 MSDSLVCEVDPETELKRFKRETDNAIITKVKDROMVYLEEFONISPEELKME 60
Db 1 MSDSLVCEVDPETELKRFKRETDNAIITKVKDROMVYLEEFONISPEELKME 60
Oy 61 LPEROPRFVYVSYKYVHDDGVSYPICFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120
Db 61 LPEROPRFVYVSYKYVHDDGVSYPICFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120

RESULT 3
O9BS35 PRELIMINARY; PRT; 154 AA.
ID O9BS35;
AC O9BS35;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Gila maturation factor, beta.
GN Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Bladder;
RC Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005359; AAH05359.1; -
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; cofillin_ADF.1.
DR SMART; SM00102; ADF.1.
SO SEQUENCE 154 AA; 18110 MW; 712DB64F30E530FD CRC64;

Query Match 84.6%; Score 622; DB 4; Length 154;
Best Local Similarity 82.3%; Pred. No. 5.9e-53;
Matches 116; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

Oy 1 MSDSLVCEVDPETELKRFKRETDNAIITKVKDROMVYLEEFONISPEELKME 60
Db 1 MSELVVCDAVEDLVEKRLFRFRKRTNNAIITKIDKRLVLDLEBSIDELKDE 60
Oy 61 LPEROPRFVYVSYKYVHDDGVSYPICFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120
Db 61 LPEROPRFVYVSYKYVHDDGVSYPICFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120

Oy 121 FEIRTTDLTEAWLOEKLSFFR 142
Db 121 FEIRTTDLTEAWLOEKLSFFR 142

RESULT 4
O9ERL8 PRELIMINARY; PRT; 142 AA.
ID O9ERL8;
AC O9ERL8;
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Gila maturation factor-beta.
GN GMEB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss/TOPI OF1; TISSUE=Telencephalon;
RC Bourgeois F., Guilmet F., Mas C., Bulfone A., Levacher B.,
RA Moalic J.M., Simonneau M.;
RT "Identification and isolation of a full-length clone of mouse GMEB
RT (Gmfb), a putative intracellular kinase regulator, differentially
RT expressed in telencephalon."
RT Cytogenet. Cell Genet. 92:304-309(2001).
DR EMBL: AF297220; AAC22803.1; -
DR MGD; MGI:1927133; Gmfb.
DR InterPro; IPR002108; Actbind_cofin.
DR Pfam; PF00241; cofillin_ADF.1.
```


OS *Drosophila melanogaster* (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 ON NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champs M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mkios G.L.G.,
 RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.T., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Dudin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaeser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibgwan C.,
 RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.R., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lal Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Melnikov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nussken D.R., Pacle J.M.,
 RA Palazolo M., Plittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shie B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC Celniker S.E., Adams M.D., Kronmiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Bazon J., An H., Baldwin D., Bazon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champs M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galie R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Idegawa C., Jatali M., Kruse D., Li P., Matel B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nuno J.,
 RA Pacle J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clump M., Drysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Kronmiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Seear S.M.J., Smith E., Shu S., Smitnik F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;

RT "Annotation of *Drosophila melanogaster* genome.";
 RL submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RX MEDLINE=99403001; PubMed=10471707;
 RA Ashburner M., Misra S., Roote J., Lewis S.E., Blazey R., Davis T.,
 RA Doyle C., Galie R., George R., Harris N., Hartzell G., Harvey D.,
 RA Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A.,
 RA Palazolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitehead K.,
 RA Celniker S., Rubin G.M.;
 RT "An exploration of the sequence of a 2.9-Mb region of the genome of
Drosophila melanogaster: the Adh region.";
 RL Genetics 153:179-219(1999).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Berkeley;
 RA Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazey R.G.,
 RA Buteonoff C., Champs M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
 RA Farfan D.E., Galie R., George R.A., Harris N.L., Hoskins R.A.,
 RA Houston K.A., Hummasti S.R., Karra K., Keane L., Kim E., Lee B.,
 RA Lewis S., Li P., Lomolan M.A., Mazda P., Moshrefi A., Nixon K.,
 RA Pacle J., Park S., Pfeiffer B., Poon L., Sequelra A.,
 RA Sechi H., Snir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R.,
 RA Zieran L.L., Rubin G.M.;
 RL submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003650; AAF53517.2;
 DR EMBL; AE003415; AAF4999.1;
 DR FlyBase; FBgn0028894; BG:DS02740.9.
 DR InterPro; IPR002108; Actbind_cofin.
 DR Pfam; PF00241; cofin_1.
 DR SMART; SM00102; ADF_1.
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 AC Q17247;
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 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
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 GN BmGF.
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 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Onchocercidae; Brugia.
 ON NCBI_TaxID=6279;
 RN [1]

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DR SMART; SM00102; ADF; 1.  
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Query match 23.88; Score 175; DB 3; Length 141;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 23, 2003, 15:08:53 ; Search time 30 Seconds

(Without alignments)
200.271 Million cell updates/sec

Title: US-10-004-832-2

Perfect score: 735
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Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents-AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	735	100.0	142	2	US-08-187-186A-2
2	735	100.0	142	2	US-08-442-497C-2
3	735	100.0	142	4	US-09-333-033-2
4	735	100.0	142	5	PCT-US94-05186-2
5	723	98.4	142	4	US-09-663-600A-229
6	622	84.6	141	4	US-09-333-033-9
7	618	84.1	141	2	US-08-187-186A-5
8	614	83.5	141	2	US-08-442-497C-9
9	558	75.9	109	4	US-09-663-600A-213
10	513	15.4	350	1	US-08-184-252A-2
11	513	15.4	350	2	US-09-123-851-3
12	513	15.4	350	2	US-08-728-520-3
13	513	15.4	350	5	PCT-US95-00601-2
14	106.5	14.5	357	2	US-09-123-851-4
15	106.5	14.5	357	2	US-08-728-520-4
16	103	14.0	343	2	US-09-123-851-1
17	103	14.0	343	2	US-08-728-520-1
18	84.5	11.5	496	4	US-09-107-532A-1164
19	75	10.2	308	4	US-09-134-001C-4400
20	72	9.8	1678	4	US-09-535-008-69
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22	72	9.8	1681	4	US-09-535-008-77
23	72	9.8	1682	4	US-09-535-008-73
24	71	9.7	686	4	US-09-107-532A-5118
25	71	9.7	646	4	US-09-535-008-67
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29	69	9.4	254	3	US-09-318-448-25	Sequence 25, Appl
30	69	9.4	428	4	US-09-134-001C-2942	Sequence 2942, Ap
31	69	9.4	793	4	US-09-107-532A-5141	Sequence 5141, Ap
32	68.5	9.3	433	4	US-09-595-424-2	Sequence 2, Appl1
33	68.5	9.3	494	4	US-09-595-424-4	Sequence 4, Appl1
34	68.5	9.3	658	4	US-09-595-424-6	Sequence 6, Appl1
35	68	9.3	454	3	US-08-764-870-5	Sequence 5, Appl1
36	68	9.3	454	3	US-08-980-115-5	Sequence 5, Appl1
37	68	9.3	454	6	5260432-2	Patent No. 5260432
38	68	9.3	783	6	5231168-2	Patent No. 5231168
39	67.5	9.2	887	4	US-09-328-352-4479	Sequence 4479, Ap
40	67.5	9.2	1151	4	US-09-328-352-5876	Sequence 5876, Ap
41	67	9.1	1169	4	US-09-255-828-20	Sequence 20, Appl
42	66.5	9.0	251	4	US-09-286-981B-4	Sequence 4, Appl1
43	66.5	9.0	307	4	US-09-075-460-16	Sequence 16, Appl
44	66.5	9.0	414	4	US-09-286-981B-10	Sequence 10, Appl
45	66.5	9.0	564	3	US-09-308-022-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-187-186A-2
Sequence 2, Application US/08187186A
Patent No. 5922572
GENERAL INFORMATION:
APPLICANT: Craig A. Rosen; Henrik Olsen;
APPLICANT: Mark D. Adams; and Ewen Kirkness
TITLE OF INVENTION: HAEMOPOIETIC MATURATION FACTOR
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,186A
FILING DATE: January 25, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-46 (PF105)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-187-186A-2

Query Match 100.0%; Score 735; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 2, 5e-83;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-08-442-497C-2
Sequence 2, Application US/08442497C
Patent No. 5986069
GENERAL INFORMATION:
APPLICANT: KIRKNESS, ET AL.
TITLE OF INVENTION: Human Haemopoietic Maturation
TITLE OF INVENTION: Factor
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,497C
FILING DATE: Concurrently
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,186
FILING DATE: 25 JAN 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05186
FILING DATE: 10 MAY 1994
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-282 (PF105P1)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 142 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-442-497C-2

Query Match 100.0%; Score 735; DB 2; Length 142;
Best Local Similarity 100.0%; Pred. No. 2, 5e-83;
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RESULT 3
US-09-333-033-2
Sequence 2, Application US/09333033
Patent No. 6346246
GENERAL INFORMATION:
APPLICANT: Kirkness et al.
TITLE OF INVENTION: Human Haemopoietic Maturation Factor
FILE REFERENCE: PF105PID1
CURRENT APPLICATION NUMBER: US/09/333,033
CURRENT FILING DATE: 1999-06-15
PRIOR APPLICATION NUMBER: 08/442,497
PRIOR FILING DATE: 1995-05-16
PRIOR APPLICATION NUMBER: 08/187,186
PRIOR FILING DATE: 1994-01-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 142
TYPE: PRT
ORGANISM: Homo sapiens
US-09-333-033-2

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Best Local Similarity 100.0%; Pred. No. 2, 5e-83;
Matches 142: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4
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Sequence 2, Application PC/TUS9405186
GENERAL INFORMATION:
APPLICANT: KIRKNESS, ET AL.
TITLE OF INVENTION: Haemopoietic Maturation Factor
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/187,186
FILING DATE: 25 JANUARY 1994
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 325800-46
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700

APPLICATION NUMBER: US/08/187,186A
FILING DATE: January 25, 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073


```

SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/123,851
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/728,520
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0136 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 451482
US-09-123-851-3

Query Match 15.4%; Score 113; DB 2; Length 350;
Best Local Similarity 26.4%; Pred. NO. 1.2e-05;
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QY 117 --LTKVFEIRTTDDLTLEAMLOEKL 138
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Db 289 MDVIRKIEIDNGDELTADELVEEV 312

RESULT 12
US-08-728-520-3
: Sequence 3, Application US/08728520
: Patent No. 5994112
: GENERAL INFORMATION:
: APPLICANT: Goll, Surya K.
: TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: U.S.
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FASTSEQ Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/728,520
: FILING DATE: Filed Herewith
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0136 US

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 451482
US-08-728-520-3

Query Match 15.4%; Score 113; DB 2; Length 350;

Best Local Similarity 26.4%; Pred. No. 1.2e-05;

Matches 38; Conservative 33; Mismatches 53; Indels 20; Gaps 7;

QY 6 VCEVDPELTETKLRFRKRTDAAITMKYDKRQWVLEEFQNTSPPELKMELPERQ 65
DB 178 VAFPIRRAFALEKLNRLNRLN---YVQLEIDIKNEIIL---ANTNTLEK-DLPKRI 229
QY 66 P-----REVVISYKYVHDDGRVSYPLCFIFSSP-VGCKPEQOMYAGSKNRLVQTAE--- 116
DB 230 PKDSARYHFFLYKSHH-EGDYLESIVFIYSPGYTCSIRERMLVSSCKSRLEIYERQ 288
QY 117 --LTKVFEIRTTDDLEAMLOEKL 138
DB 289 MDVIRKIEIDNGDELTADELFEYEV 312

RESULT 13
PCT-US95-00601-2

Sequence 2, Application PC/TUS9500601
GENERAL INFORMATION:
APPLICANT: United States of America Department of Health and Human
APPLICANT: Services
TITLE OF INVENTION: PROTEIN TYROSINE KINASE A6
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knodbe, Martens Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
CITY: Newport Beach
STATE: CA
COUNTRY: USA
ZIP: 92260
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/00601
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH084.001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 350 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-00601-2

Query Match 15.4%; Score 113; DB 5; Length 350;

Best Local Similarity 26.4%; Pred. No. 1.2e-05;

Matches 38; Conservative 33; Mismatches 53; Indels 20; Gaps 7;

QY 6 VCEVDPELTETKLRFRKRTDAAITMKYDKRQWVLEEFQNTSPPELKMELPERQ 65
DB 178 VAFPIRRAFALEKLNRLNRLN---YVQLEIDIKNEIIL---ANTNTLEK-DLPKRI 229
QY 66 P-----REVVISYKYVHDDGRVSYPLCFIFSSP-VGCKPEQOMYAGSKNRLVQTAE--- 116
DB 230 PKDSARYHFFLYKSHH-EGDYLESIVFIYSPGYTCSIRERMLVSSCKSRLEIYERQ 288
QY 117 --LTKVFEIRTTDDLEAMLOEKL 138
DB 289 MDVIRKIEIDNGDELTADELFEYEV 312

RESULT 14

US-09-123-851-4

Sequence 4, Application US/09123851

Patent No. 5958405

GENERAL INFORMATION:

APPLICANT: Goli, Surya K.

TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/123,851

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/728,520

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0136 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 357 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: GenBank

CLONE: 1166579

US-09-123-851-4

Query Match 14.5%; Score 106.5; DB 2; Length 357;

Best Local Similarity 22.8%; Pred. No. 7.6e-05;

Matches 37; Conservative 30; Mismatches 60; Indels 35; Gaps 5;

QY 6 VCEVDPELTETKLRFRKRTDAAITMKYDKRQWVLEEFQNTSPPELKMELPERQ 65
DB 171 VAFVDRAAEALRQLASQK---LSFYQSVDTLNEAIKIEGTLESLEPSQASKVPDK 227
QY 66 PRFVVISYKYVHDDGRVSYPLCFIFSSP-VGCKPEQOMYAGSKNRLVQTAE----- 116
DB 228 PRFTFYNDRTW-EGVPOQCTLFTYSLPSSGSSIKERLTVSSCKGPFPLSAONQYVIT 286
QY 117 -----LTKVFEIR-----TTDDLEAMLOEKL 136

Db 287 NKFLQKRSNKKFKIRKIFLKLKNDMEVDARDLSEKALLE 328

RESULT 15

US-08-728-520-4

; Sequence 4, Application US/08728520

; Patent No. 5994112

; GENERAL INFORMATION:

; APPLICANT: GOLI, Surya K.

; TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FASTSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/728,520

; FILING DATE: Filed Herewith

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 357 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 116579

; US-08-728-520-4

Query Match 14.5%; Score 106.5; DB 2; Length 357;

Best Local Similarity 22.8%; Pred No. 7.6e-05;

Matches 37; Conservative 30; Mismatches 60; Indels 35; Gaps 5;

OY 6 VCEVDPELTETKLRFRFRKETDAAIIMKYDKDQWVLEEFQNTSPSELKMLPERQ 65
Db 171 VAFPDVRAAEALROLASQ--LSFVQLSVDTLNEAIKLEGTLESLPQLASKVPRDK 227
OY 66 PRFVYISKYVHDGSRVYPLCFIFSSP-VGCKPEQOMYAGSKNRIVQTAE----- 116
Db 228 PRYTFYNPDHW-BGVPOQCTLFYSLPSSGSSIKERMLYSSCKGPFILSAONQYGVYT 286
OY 117 -----LTKVFEIR-----TTDDLTFAWLOE 136
Db 287 NKFLQKRSNKKFKIRKIFLKLKNDMEVDARDLSEKALLE 328

Search completed: September 23, 2003, 15:13:01
Job time : 31 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 23, 2003, 15:07:23 : Search time 27 Seconds

(without alignments)
783.069 Million cell updates/sec

Title: US-10-004-832-2

Perfect score: 735

Sequence: 1 MSDSLVCEVDEPDELTEKLRK.....IRTTDDLEAWLOEKLSPFR 142

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 556269 seqs, 148893369 residues

Total number of hits satisfying chosen parameters: 556269

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*

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2: /cgn2_6/ptodata/1/pubpaa/PC1_NEW_PUB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	735	100.0	142	14	US-10-004-832-2
2	723	98.4	142	12	US-10-319-763-229
3	699	95.1	147	9	US-09-925-302-642
4	614	83.5	141	14	US-10-004-832-9
5	558	75.9	109	12	US-10-319-763-213
6	113	15.4	350	11	US-09-251-225-3
7	113	15.4	350	15	US-10-037-340-266
8	113	15.4	350	15	US-10-205-823-241
9	113	15.4	385	9	US-09-925-299-966
10	113	15.4	385	11	US-09-925-299-966
11	113	15.4	385	15	US-10-106-698-4598
12	109.5	14.9	224	14	US-10-108-605-277
13	108	14.7	348	10	US-09-969-384-19
14	106.5	14.5	357	11	US-09-251-225-4
15	103	14.0	343	11	US-09-251-225-1

16	78.5	10.7	166	15	US-10-205-342-21	Sequence 21, Appl
17	78.5	10.7	166	15	US-10-205-823-72	Sequence 72, Appl
18	74.5	10.1	487	11	US-09-298-523B-66	Sequence 66, Appl
19	71.5	9.7	722	15	US-10-029-495-5	Sequence 5, Appl
20	71	9.7	1647	11	US-09-824-574-4	Sequence 4, Appl
21	70.5	9.6	299	9	US-09-815-242-10563	Sequence 10563, A
22	70.5	9.6	487	11	US-09-298-523B-9	Sequence 9, Appl
23	69.5	9.5	685	9	US-09-801-574-6	Sequence 6, Appl
24	69	9.4	310	10	US-09-925-300-1602	Sequence 1602, Ap
25	68.5	9.3	189	11	US-09-764-891-3897	Sequence 3897, Ap
26	68.5	9.3	454	9	US-09-764-881-148	Sequence 148, Ap
27	68	9.3	454	9	US-09-797-727-2	Sequence 2, Appl
28	68	9.3	454	11	US-09-814-604-3	Sequence 3, Appl
29	67.5	9.2	148	14	US-10-108-605-27	Sequence 27, Appl
30	67.5	9.2	911	15	US-10-204-887-123	Sequence 123, Ap
31	67	9.1	440	11	US-09-910-186A-8	Sequence 8, Appl
32	67	9.1	1169	12	US-10-241-596-20	Sequence 20, Appl
33	67	9.1	1713	15	US-10-270-333-177	Sequence 177, Ap
34	66.5	9.0	168	9	US-09-945-301-5	Sequence 5, Appl
35	66.5	9.0	251	12	US-10-254-995-4	Sequence 4, Appl
36	66.5	9.0	254	11	US-09-056-019-9	Sequence 9, Appl
37	66.5	9.0	307	12	US-10-216-667-16	Sequence 16, Appl
38	66.5	9.0	326	9	US-09-841-132-585	Sequence 585, Ap
39	66.5	9.0	376	11	US-09-056-019-7	Sequence 7, Appl
40	66.5	9.0	413	11	US-09-056-019-35	Sequence 35, Appl
41	66.5	9.0	414	12	US-10-254-995-10	Sequence 10, Appl
42	66.5	9.0	481	11	US-09-298-523B-6	Sequence 6, Appl
43	66.5	9.0	483	11	US-09-298-523B-10	Sequence 10, Appl
44	66.5	9.0	539	11	US-09-298-523B-54	Sequence 54, Appl
45	66.5	9.0	581	11	US-09-298-523B-56	Sequence 56, Appl

ALIGNMENTS

RESULT 1		US-10-004-832-2	
Sequence 2, Application US/10004832			
Publication No. US20020146408A1			
GENERAL INFORMATION:			
APPLICANT: Kirkness et al.			
TITLE OF INVENTION: Human Haemopoietic Maturation Factor			
FILE REFERENCE: PFI05PID2			
CURRENT APPLICATION NUMBER: US/10/004,832			
CURRENT FILING DATE: 2001-12-07			
PRIOR APPLICATION NUMBER: US 09/333,033			
PRIOR FILING DATE: 1999-06-15			
PRIOR APPLICATION NUMBER: US 08/442,497			
PRIOR FILING DATE: 1995-05-16			
PRIOR APPLICATION NUMBER: US 08/187,186			
PRIOR FILING DATE: 1994-01-25			
NUMBER OF SEQ ID NOS: 9			
SOFTWARE: PatentIn version 3.1			
SEQ ID NO 2			
LENGTH: 142			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-10-004-832-2			
Query Match		100.0%; Score 735; DB 14; Length 142;	
Best Local Similarity		100.0%; Pred. No. 5.1e-75;	
Matches 142; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	1	MSDSLVCVDEPDELTEKLRKFRKRETDNAITMKVVDKRDQMYVEEEOITSPBELKME	60
DB	1	MSDSLVCVDEPDELTEKLRKFRKRETDNAITMKVVDKRDQMYVEEEOITSPBELKME	60
QY	61	LPEROPRVVYSYKVVHDGRVSYPLCFSSPVCKPBDQMMYAGSKNRILVOTAEIKRV	120
DB	61	LPEROPRVVYSYKVVHDGRVSYPLCFSSPVCKPBDQMMYAGSKNRILVOTAEIKRV	120
QY	121	FEIRTTDDLEAWLOEKLSPFR 142	
DB	121	FEIRTTDDLEAWLOEKLSPFR 142	

Db 121 FEIRTTDDLTEAMLQEKLSFFR 142

RESULT 2

US-10-319-763-229

Sequence 229, Application US/10319763

Publication No. US20030144490A1

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Duclert, Aymeric

APPLICANT: Bougueleret, Lydie

TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS

FILE REFERENCE: G-031.US04.DIV

CURRENT FILING DATE: US/10/319,763

PRIOR FILING DATE: 2002-12-10

PRIOR APPLICATION NUMBER: 60/066,677

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/069,957

PRIOR FILING DATE: 1997-12-17

PRIOR APPLICATION NUMBER: 60/074,121

PRIOR FILING DATE: 1998-02-09

PRIOR APPLICATION NUMBER: 60/081,563

PRIOR FILING DATE: 1998-04-13

PRIOR APPLICATION NUMBER: 60/096,116

PRIOR FILING DATE: 1998-08-10

PRIOR APPLICATION NUMBER: 60/099,273

PRIOR FILING DATE: 1998-09-04

NUMBER OF SEQ ID NOS: 229

SOFTWARE: Patent.pm

SEQ ID NO 229

LENGTH: 142

TYPE: PRT

ORGANISM: Homo sapiens

US-10-319-763-229

Query Match 98.4%; Score 723; DB 12; Length 142;

Best Local Similarity 98.6%; Pred. No. 1,2e-73;

Matches 140; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSDSLVYCEVDPPELTETKRFRRKFTDNAAIIKVKDKROMVYLEEFQNISPEELKME 60

Db 1 MSDSLVYCEVDPPELTETKRFRRKFTDNAAIIKVKDKROMVYLEEFQNISPEELKME 60

QY 61 LPERQPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120

Db 61 LPERQPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120

QY 121 FEIRTTDDLTEAMLQEKLSFFR 142

Db 121 FEIRTTDDLTEAMLQEKLSFFR 142

RESULT 3

US-09-925-302-642

Sequence 642, Application US/09925302

Patent No. US20020044941A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REFERENCE: PA104

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR FILING DATE: 2000-03-08

PRIOR APPLICATION NUMBER: 60/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 642

LENGTH: 147

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SITE

LOCATION: (2)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (103)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

US-09-925-302-642

Query Match 95.1%; Score 699; DB 9; Length 147;

Best Local Similarity 99.3%; Pred. No. 6.1e-71;

Matches 135; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 VCEVDPPELTETKRFRRKFTDNAAIIKVKDKROMVYLEEFQNISPEELKMELEPEROP 66

Db 12 VCEVDPPELTETKRFRRKFTDNAAIIKVKDKROMVYLEEFQNISPEELKMELEPEROP 71

QY 67 RFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKVFEIRTT 126

Db 72 RFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKVFEIRTT 131

QY 127 DDLTEAMLQEKLSFFR 142

Db 132 DDLTEAMLQEKLSFFR 147

RESULT 4

US-10-004-832-9

Sequence 9, Application US/10004832

Publication No. US20020146408A1

GENERAL INFORMATION:

APPLICANT: Kirkness et al.

TITLE OF INVENTION: Human Haemopoietic Maturation Factor

FILE REFERENCE: PF105PID2

CURRENT APPLICATION NUMBER: US/10/004,832

CURRENT FILING DATE: 2001-12-07

PRIOR APPLICATION NUMBER: US 09/333,033

PRIOR FILING DATE: 1999-06-15

PRIOR APPLICATION NUMBER: US 08/442,497

PRIOR FILING DATE: 1995-05-16

PRIOR APPLICATION NUMBER: US 08/187,186

PRIOR FILING DATE: 1994-01-25

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin version 3.1

SEQ ID NO 9

LENGTH: 141

TYPE: PRT

ORGANISM: Homo sapiens

US-10-004-832-9

Query Match 83.5%; Score 614; DB 14; Length 141;

Best Local Similarity 81.6%; Pred. No. 2.2e-61;

Matches 115; Conservative 15; Mismatches 11; Indels 0; Gaps 0;

QY 1 MSDSLVYCEVDPPELTETKRFRRKFTDNAAIIKVKDKROMVYLEEFQNISPEELKME 60

Db 1 MSELVYCDVAEDVLEKTRFRFRKFTDNAAIIKVKDKRLVYLDLELGISPEELKME 60

QY 61 LPERQPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120

Db 61 LPERQPRFVYVSYKYVHDDGRVSYPLCFIFSSPVGCKPEQOMYAGSKNRLVQTAELTKV 120

QY 121 FEIRTTDDLTEAMLQEKLSFFR 141

Db 121 FEIRTTDDLTEAMLQEKLSFFR 141

RESULT 5

US-10-319-763-213

Sequence 213, Application US/10319763

Publication No. US20030144490A1

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, Jean-Baptiste

APPLICANT: Duclert, Aymeric

```
APPLICANT: Bouguetel, Lydie
TITLE OF INVENTION: EXTENDED CDNAS FOR SECRETED PROTEINS
FILE REFERENCE: G-031.US04.DIV
CURRENT APPLICATION NUMBER: US/10/319,763
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: 60/066,677
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/069,957
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/074,121
PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/081,563
PRIOR FILING DATE: 1998-04-13
PRIOR APPLICATION NUMBER: 60/096,116
PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/099,273
PRIOR FILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 229
SOFTWARE: Patent.pm
SEQ ID NO 213
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-10-319-763-213

Query Match
Best Local Similarity 98.2%; Score 558; DB 12; Length 109;
Matches 107; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 34 MKVDKROMVLEEFONISPEELKMLPEROPREVVYSGKYVHDDGRVSYPLCFITSSP 93
DB 1 MKVDKROMVLEEFONISPEELKMLPEROPREVVYSGKYVHDDGRVSYPLCFITSSP 60
QY 94 VCKPEQOMYAGSKNRLVQTAELTYVEIRTTDTLTEAMLOEKLSFFR 142
DB 61 VCKPEQOMYAGSKNRLVQTAELTYVEIRTTDTLTEAMLOEKLSFFR 109

RESULT 6
US-09-251-225-3
Sequence 3, Application US/09251225
Publication No. US20030099652A1
GENERAL INFORMATION:
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/251,225
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0136 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0535
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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LENGTH: 350 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 451482
US-09-251-225-3

Query Match
Best Local Similarity 15.4%; Score 113; DB 11; Length 350;
Matches 38; Conservative 33; Mismatches 53; Indels 20; Gaps 7;

QY 6 VVCENDPELTERKFRFRKEDNNAIIMKVDKROMVLEEFONISPEELKMLPERO 65
DB 178 VAFPSREAFQALEKNNRQLN--YVQLEIDIKKEIIL--ANTWTLEIK-DLPKRI 229
QY 66 P----REVVYSGKYVHDDGRVSYPLCFITSSP-VGCKPEQOMYAGSKNRLVQTAE---- 116
DB 230 PKDSARYHFFLKHSB-EGDYLESIVFTISMPGYTCSTIRKMLYSSCKSRLEIYERQ 288
QY 117 --LTKVFEIRTTDTLTEAMLOEKL 138
DB 289 MDVIRKIEIDNGDELTADELFLYEYEV 312

RESULT 7
US-10-097-340-266
Sequence 266, Application US/10097340
Publication No. US20030087250A1
GENERAL INFORMATION:
APPLICANT: John MONAHAN
APPLICANT: Manjula GANNAVAPU
APPLICANT: Sebastian HOERSCH
APPLICANT: Shubhangi KAMATKAR
APPLICANT: Steve G. KOVATS
APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISBY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter WEIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, JR.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMANDT
APPLICANT: Xumei ZHAO
APPLICANT: Karen GIATTI
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
Assessment, Prevention, and Therapy of Ovarian Cancer
FILE REFERENCE: MRI-030
CURRENT APPLICATION NUMBER: US/10/097,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 266
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
```


APPLICANT: GOLI, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/251,225
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0136 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1166579
US-09-251-225-4

Query Match 14.5%; Score 106.5; DB 11; Length 357;
Best Local Similarity 22.8%; Pred. No. 0.0012;
Matches 37; Conservative 30; Mismatches 60; Indels 35; Gaps 5;

QY 6 VCEVDPELTLEKLRFRFRKETDANAIIIMKYDKDROMVLEEFONISPEELKMELEPERQ 65
DB 171 VAFVDRNAEALQLASQK---LSFVQLSVDTLNEAIKLEGTLESLEPSQLASKVPRDK 227
QY 66 PRFVVSYSKYVHDGRVSYPLCFITFSSP-VGCKPEQOMVAGSKNRLVQTAE----- 116
DB 228 PRYTFYNEDHTW-EGVPOQCTLFITYSLPSSGSSIKERMLYSSCKGPFLSAONQYGVYIT 286
QY 117 -----LTQVEIR-----TTDDLTFAWLOE 136
DB 287 NKFLQKRSNKMFKIREKIFELRLKNDMEVDARDLSEKALLE 328

RESULT 15
US-09-251-225-1
Sequence 1, Application US/09251225
Publication No. US20030099652A1
GENERAL INFORMATION:
APPLICANT: GOLI, Surya K.
TITLE OF INVENTION: A NOVEL HUMAN PROTEIN TYROSINE KINASE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/251,225
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0136 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY:
CLONE: Consensus
US-09-251-225-1

Query Match 14.0%; Score 103; DB 11; Length 343;
Best Local Similarity 26.4%; Pred. No. 0.0028;
Matches 37; Conservative 32; Mismatches 51; Indels 20; Gaps 7;

QY 10 VDPELTLEKLRFRFRKETDANAIIIMKYDKDROMVLEEFONISPEELKMELEPERQ--- 66
DB 182 LQPAQRLAQLD---KQNMVYIQMKLDLERET---ELVHTPTDY-AQLPRVVRDA 233
QY 67 -RFVVSYSKYVHDGRVSYPLCFITFSSP-VGCKPEQOMVAGSKNRLVQTAE-----ELT 118
DB 234 ARYHXPFLYKHNH-EGDPLESVFLYSPMGYKCSIKERMLYSSCKSRLLDSVEQDFHLEIA 292
QY 119 KVEIRTTDLTEAWLOEKL 138
DB 293 KKIEIGGAELTAELFYDEV 312

Search completed: September 23, 2003, 15:12:24
Job time : 28 secs